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//ggn_2_6/ptodata///ina/Sh_COMB.seq:US-08-78-533-2 992.00 2000.38 3.46-10 575 (2002.06) ptodata//ina/Sh_COMB.seq:US-08-78-533-2 992.00 2000.38 3.46-10 575 (2002.06) ptodata//ina/Sh_COMB.seq:US-08-78-533-2 992.00 2000.38 3.46-10 575 (2002.06) ptodata//ina/Sh_COMB.seq:US-08-64-70-793-1 424.50 874.11 5.3e-41 926 (2002.06) ptodata//ina/Sh_COMB.seq:US-08-78-793-1 424.50 874.11 5.3e-41 926 (2002.06) ptodata//ina/Sh_COMB.seq:US-09-787-793-1 424.50 874.11 5.3e-41 926 (2002.06) ptodata//ina/Sh_COMB.seq:US-09-323-773-1 424.50 874.11 5.3e-41 926 (2002.06) ptodata//ina/Sh_COMB.seq:US-08-65-485A-20 406.50 88.91 4.9e-39 717 (2002.06) ptodata//ina/Sh_COMB.seq:US-08-65-485A-20 406.50 88.91 4.9e-39 717 (2002.06) ptodata//ina/Sh_COMB.seq:US-08-65-485A-19 406.50 88.91 4.9e-39 717 (2002.06) ptodata//ina/Sh_COMB.seq:US-09-080-285-04 406.50 88.91 4.9e-39 717 (2002.06) ptodata//ina/Sh_COMB.seq:US-09-080-285-19 406.50 88.91 4.9e-39 717 (2002.06) ptodata//ina/Sh_COMB.seq:US-09-080-325-10 406.50 88.50 88.91 4.9e-39 708 (2002.06) ptodata//ina/Sh_COMB.seq:US-09-080-325-10 406.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.50 88.5
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-MODEL-frame+_p2n.model -DEV=xlh
-Q-/Ggn2_1/USPTO_spool/US9915327/runat_06062002_084852_18504/app_query.fasta_1.508
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-DB-Issued_Patents_NA -OFMT=fatap -SUFFIX=P2n.rni
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-USER=US09155327_@CGN1_1118-NCPU=6 -ICPU=3 -LONGIGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       About: Results were produced by the GenCore software, version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: Jun 6, 2002 2:32 PM
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Query length: 193
Database: Issued_Patent
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Database sequences: 383533
Database length: 122816752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search time (sec): 65.480000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strd Orig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-798-897-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Apprix
Sequence 1, S789201
                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.192
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-798-897-1 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                         US-09-155-327E-9 x US-08-798-897-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Guaste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Genes Codi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0/
                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                   51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                         51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                              17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
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                                                                                                                                                                                                                                               1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                      1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
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                                                              GGGAAGGCCCAGCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA
20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Esmond, Robert W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KESSLER, GOLDSTEIN & FOX P.L.L.C.
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                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 98.964
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seq_documentation_block:
; Sequence 1, Application US/08978523
; Patent No. 5883229
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TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                     NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Guaste
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
ADDERSCENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 GCCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGGCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT 400
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                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 New
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20005
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                                                                                                        1483.0140002
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-798-897-2
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US-09-155-327E-9 x US-08-978-523-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 100.000
                                         551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                             184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                    501 GCCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGCCCTGG 550
                                                                                                                                          167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                   451 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                              151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                       134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GTCTTTGGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 GCTACACGTGACCCCAGGCTCAGCCCAGCCAACGCTTCACCCAGGTTTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 579 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                          ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1002.00
Ratio: 5.192
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                                                                                                                                                                                                                                                                                                                                                                          400
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Sequence 2, Application US/08798897 Patent No. 5789201 GENERAL INFORMATION:

APPLICANT:

Guastella, John

seq\_documentation\_block:

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MOLECULE TYPE:
US-08-798-897-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-155-327E-9 x US-08-798-897-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio: 5.167 Gaps: 0
percent Similarity: 99.482 Percent Identity: 97.927
                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-798-897-2 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Genes Codi
TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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                                                                                                                                                                                                                                                  201 GCTGCATGTGACCCCAGGCTCAGCCCAACGCTTCACCCAGGTCTCCG 250
                                                                                                                                                                                       151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                 51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                              251 ATGAACTITTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                  51 AspGlupheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 579 base pairs
                                                                                                                                                       67 nLeuHisvalThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                         1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValalaAspPh 17
                                                                              84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                            1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-523-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08978523 Patent No. 5883229 GENERAL INFORMATION:
APPLICANT: Guastella, John
                                                                                           ; TOPOLOGY: bo
; MOLECULE TYPE:
US-08-978-523-2
                             alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 eualaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAAGGGGAACTG 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/978,523
APPLICATION NUMBER: US/08/978,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Genes Codi
                                                                                                                                                                                                                TELEFAX: 202-3/1-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:
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                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                nucleic acid
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1100 New York Avenue, N.W., Suite 600
                     Ratio:
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202-371-2540
                                                                                                                                    both
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                                                                                                                      CDNA
                                                                                                                                                    both
       5.167
99.482
                                      992.00
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       Percent Identity: 97.927
                                                                                                                                                                                                                                                                                      1483.0140002
                                             Length:
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alignment\_block: US-09-155-327E-9 x US-08-978-523-2

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Sequence 5, Application US/08081448
Patent No. 5646008
GENERAL INFORMATION:
APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-081-448-5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-978-523-2 from: 1 to: 579
                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                             STREET: SIL
                                                                                                                                                                                                                                                                                                                                                                              551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                 184 alThrvalGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                            501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGGACTGGGGGCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                            COUNTRY: UZIP: 60610
                                                                               ADDRESSEE: Arnold, white a purpose STREET: 321 No. 5646008th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG1 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 424.50 Length: 224
Ratio: 2.989 Gaps: 4
Percent Similarity: 63.393 Percent Identity: 40.179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
500 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC 549
                                                                                                                                       450 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 499
                                                                                                                                                                                                          400 CCCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTC 449
                    95 rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                                                                                                                                                                                                             350 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGCAAG 399
                                                                                           78 gPheThrGlnvalSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                          62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                                                300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 349
                                                                                                                                                                                                                                                                                                                                                                                                                   250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                              45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                              41 .....ProLeuHisGlnA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 ............GlyGluGlyProAlaAlaAsp......40
                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 .....ValCysGlyAlaGlypro 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: No. 5646008thrup, Thorage Trafion Number: 3,268
REFERENCE/DOCKET NUMBER: ARGETELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: No. 5646008thrun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
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LOCATION: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 19930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Balance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARCD090
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alignment_scores:
                                                US-08-470-670A-6
                                                                             FEATURE:
                                                         NAME/KEY:
LOCATION:
                                                                                      TOPOLOGY:
                                                                                                STRANDEDNESS:
Quality:
Ratio:
                                                          CDS
135..836
                                                                                       linear
  424.50
2.989
                                                                                                 single
            Length:
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-470-670A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08470670A Patent No. 5834309 Patent No. 5834309 5710045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                               TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 AsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetValAl 128 :::|||||||||:::: |||||||:::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 laGlupheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  800 CGTGGTTCTGCTGGGCTCACTC 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thompson, Craig B. B. APPLICANT: Boise, Lawrence H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                             NAME: Highlander Steven L.
REGISTRATION NUMBER: 37.642
REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                   FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
CITY: HO
STATE: T
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/081,448
                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houston
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                               US/08/470,670A
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alignment_block:
US-09-155-327E-9 x US-08-470-670A-6
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                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-481-739-1
                                                                                                                                                          seq_documentation_block:
                                                                                                             Sequence 1, Application US/08481739 Patent No. 6143291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 CGGGAGCTGGTGGCTTGACTTTCTCTCCTACAAGCTTTCCCCAGAAAGGATA 199
                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 laGlupheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                          700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                              750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                                                                                                                                                                                                                                                                           162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
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                                                                                                                                                                                                                                                                                                    176 yAlaValAlaLeuGlyAlaLeu 183
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CORRESPONDENCE ADDRESS:

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alignment_block:
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                                   397 AAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
                                                                                                        347 CAGCAGCAGTTTGGATGCCCGGGAGGTGATCCCCATGGCAGCAGTAAAGC 396
                                                                                                                                                                         300 TCCTGGCACCTGGCAGACAGCCCCGGGTGAATGGAGCC...ACTGGCCA 346
                                                                     44 lnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
                                                                                                                                                                                                                                              250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                                                                                                                   200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
                                                                                                                                                                                                                                                                                                                                                                                      150 CGGGAGCTGGTTGACTTTCTCTCTACAAGCTTTCCCCAGAAAGGATA 199
61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                                                                                                        35 uGlyProAlaAlaAsp.....ProLeuHisG 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: RP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/481,739
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                           .....ValCysGlyAlaGlyProGlyG1 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
oPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: DeConti, Giulio A. (G. REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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3.076
61.333
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alignment_block:
US-09-155-327E-9 x US-09-167-921-1
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APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
                                                                     Align seg 1/1 to: US-09-167-921-1 from: 1 to: 926
                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                         US-09-167-921-1
                                                                                                                                                                                          Percent Similarity: 63.393
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NAME/KEY: CDS

LOCATION: (135)..(836)

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: L20121 Genbank

DATABASE ENTRY DATE: 1994-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09167921A Patent No. 6172216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 1998-10-07

NUMBER: US/09/167,921A

CURRENT FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  797 CGGCGTGGTTCTGCTGGGCTCACTC 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              747 AAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGC 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 ArgLeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 ValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetVa 127
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                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                           424.50
2.989
                                                                                                                                                                               Percent Identity: 40.179
                                                                                                                                                                                                                             Length:
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150 CGGGAGCTGGTTGACTTTCTCTCCTACAAGCTTTCCCAGAAAGGATA 199

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    Patent No. 6210892
                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-277-020-39
                       SEQ ID NO 39
                                              EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
                                                                                                                 CURRENT APPLICATION NUMBER: US/09/277,020 CURRENT FILING DATE: 1999-03-26 EARLIER APPLICATION NUMBER: 09/167,921
LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 yAlaValAlaLeuGlyAlaLeu 183
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seq\_documentation\_block:

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GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: of mRNA Processing
FILE REFERENCE: ISPH-0339
FILE REFERENCE: ISPH-0339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
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                                                                                                                                                                                                                                                                                                                                                          750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
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; ORGANISM: Homo sapiens US-09-277-020-39
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US-09-155-327E-9 x US-09-277-020-39
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Percent Similarity: 63.393
seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-323-743-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 CGGGAGCTGGTGGTTGACTTTCTCTCCTACAAGCTTTCCCCAGAAAGGATA 199
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                                                                                                                                                                                                                                                      145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
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                                                                                                                             750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG
                                                                                                                                                                   162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
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                                                                                     176 yAlaValAlaLeuGlyAlaLeu 183
                                              800 CGTGGTTCTGCTGGGCTCACTC 821
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alignment_block:
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LENGTH: 926
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CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
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APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett p.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Alang, Qingqing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
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500 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC 549
                                                                                        450 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 499
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                        78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                  62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
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                                                                                                                                                                                                              45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
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2.989
63.393
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alignment_scores:
                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-08-461-511A-6
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                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 800 CGTGGTTCTGCTGGGCTCACTC 821
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| 550 GCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTA 599
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                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: ARCD:179 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Thompson, Craig B.B.

Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                        TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                            POPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Arnold, White & Durkee
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                                                                                                                    135..836
                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                               (512) 418-3000
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Quality: 424.50

Length:

224

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alignment_block:
US-09-155-327E-9 x US-08-461-511A-6
                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US94-07089-6
                                                                                                                                                             seq_documentation_block:
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                                                                            Sequence 6, Application PC/TUS9407089
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         550 GCATTGTGGCCTTTTTCTCCCTTCGGCGGGCACTGTGCGTGGAAAGCGTA 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400 CGCTGAGGGAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTC 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAG 399
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                        800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                        176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                              162 LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 .....ValCysGlyAlaGlyPro 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....ProLeuHisGlnA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGCCATGACTGTGGCCCG
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63.393
     Compositions and Methods
                                                        Vertebrate Apoptosis Gene:
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alignment_block:
US-09-155-327E-9 x PCT-US94-07089-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: PCT-US94-07089-6 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO:
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ZIP: 77210
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TYPHTER: IBM PC compatible
TYPHTER: PC-DOS/MS-DOS, ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 512-320-7200 TELEFAX: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 22 JUNE 199
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/08
FILING DATE: 22 JUNE 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: li
MOLECULE TYPE:
                                              397
                                                                                                                    347 CAGCAGCAGTTTGGATGCCCGGGAGGTGATCCCCATGGCAGCAGTAAAGC 396
                                                                                                                                                                                               300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCC...ACTGGCCA 346
                                                                                                                                                                                                                                                                           250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                                                                                                                                                    200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. BOCITY: Houston STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
                                                                                                                                                       35 uGlyProAlaAlaAsp.....ProLeuHisG 44
                                                                                                                                                                                                                                                                                                                                                                                        61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                                              44 lnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: PARKER, David L. REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: CONCUI
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                                            .....valCysGlyAlaGlyProGlyGl 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
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135..836
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3.076
61.333
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5831066
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/08465485A
                TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
                                                                                                                  FILING DATE: 22-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/124,256
FILING DATE: 20-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 rGlyAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 TTCAGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 GAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 lyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSer 110
                                                                        NAME: Fortney, Andrew D. REGISTRATION NUMBER: 34,
                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 21-FEB-1992
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/465,485A FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGC 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virginia
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ≧: P.C.
1755 S. Jefferson Davis Hwy.,
(408) 436-2075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed, John
                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBLON, SPIVAK, McCLELLAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                      05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Regulation of bcl-2 Gene Expression 29
                                                                                                                                                                                                                    US 07/840,716
                                                                                                                                                       US 07/288,692
                                                                        34,600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suite 400
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-465-485A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-155-327E-9 x US-08-465-485A-20
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  159 AlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                               528
                                                                                                                                                                                125 pMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerG 142
                                                                                                                                                                                                                        478 GAGAGCGTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTG
                                                                                                                                                                                                                                               109 GluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTr 125
                                                                                                                                                                                                                                                                                                        142 lyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGlu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 TCCACCTGGCCTCGGCCAAGCCGGCGACTTCTCCCGCCGCCGCTACCGC
                                                                                                                                                                                                                                                                                                                                                                                    378 GCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGGGTGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 GGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTGACGCCCTTCACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 TGCCCCGGCGCCGCGGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                        75 aGlnGlnArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProA 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                            92 snTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAla 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 ArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAl 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 euHisGlnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 GACAACCGGGAGATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAG
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                                                          GAGGCTGGGATGCCTTTGTGGAACTGTACGGC.........CCCAGC
                                                                                                                                          GATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGCATCCCGCGACCCGGTCGCCAGGACCTCGCCGCTGCAGACCCCGGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCCCGCACCGGGCATCTTCTCCTCCCAGCCCGGGCACACGCCCCATCCA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-080-285-20
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; Sequence 20, Application US/09080285
; Patent No. 6040181
                                                     alignment_scores:
                                                                                                               US-09-080-285-20
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666 TTTGGCCCTG...GTGGGAGCTTGCATCACCCTGGGTGCCTATCTGAGCC 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLIANCE 20-SEF 1...
FILING DATE: 20-SEF 1...
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
APPLICATION NUMBER: 21-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           713 ACAAG 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 08/124,256
APPLICATION NUMBER: US 08/124,256
APPLICATION NUMBER: US 08/124,256
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 3335-070-55 CONTTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US OF FILING DATE: 22-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                  MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arlington
STATE: Virginia
                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/080,285
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                                                                                                                                                                                                          TOPOLOGY:
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                 Quality:
Ratio:
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1..717
                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                       (408) 436-2070
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22-DEC-1988
                                                                                                                                                                                      DNA (genomic)
 406.50
2.904
59.574
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   Percent Identity: 36.596
                                         Length:
                         Gaps:
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alignment_block: us-09-155-327e-9 \times us-09-080-285-20
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                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/backfiles1.seq:5459251-1
                                                                                                                  seq_documentation_block:
                                                                                        ; Patent No. 5459251
                          ; SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 GCCGCATCCCGCGACCCGGTCGCCAGGACCTCGCCGCTGCAGACCCCGGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 CCCCGCACCGGGCATCTTCTCCTCCCAGCCCGGGCACACGCCCCATCCA 177
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278 TCCACCTGGCCCTACGCCAAGCCGGCGACGACTTCTCCCGCCGCTACCGC
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                                                 APPLICANT: TSUJIMOTO, YOShide; Croce, Carlo A. TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 AlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 ArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAl 75
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NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGCTGGGATGCCTTTGTGGAACTGTACGGC.......CCCAGC
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alignment_scores:
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                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/228,704

FILING DATE: 18-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 994,941

FILING DATE: 23-DEC-1992

APPLICATION NUMBER: 663,010

FILING DATE: 19-MAR-1991

APPLICATION NUMBER: 883,687

FILING DATE: 09-JUL-1986
1986 GATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACG 2035
                                                                                                                                                                                                                                                                                                                                                                   1836 GCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGGGTGA 1885
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Ratio:
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Gaps: 5
Percent Identity: 36.596
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OM of: US-09-155-327E-9 to: EST:*
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Query: US-09-155-327E-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database sequences: 13736207
Database length: -1841457050
Search time (sec): 2329.970000
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-DB=EST -QFMT=fastap_Suprise_153327/runat_06062002_084851_18477/app_query.fasta_1.508
-MINATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPEXT=4.000
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-EGAPEXT=7.000 -START=1 -ANATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_MSCORE=Poct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -NODE=LOCAL -OUTENT=PIS -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09155327_eCGN1_1_6527
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-NITLEN=0 -MAXLEN=2000000000 -USER=US09153327_eCGN1_1_6527
-NITLEN=0 -MAXLEN=1 -LONGLOG -DEV_TIMEOUT=120 -WARRI_TIMEOUT=30
-NO_XLEXY -WANIT -THREADS=1
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gb_est2:BE870269
gb_est2:BE870269
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                                                                                                                                                                                                                                                             gb_est2:BI457116
gb_est2:BI222971
gb_est2:BG985707
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gb_est2:BM457276
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gb_est2:BE508939
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gb_est2:BM191403
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gb_est1:AW258810
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                                                                                                                                                                                                         gb_est2:BG831301
gb_est2:BG824757
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gb_est2:BI409987
                                                      gb_est1:AW159063
gb_est2:BM193253
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9 | AK004680 Mus musculus adult ma

7 | AK004680 Mus musculus adult ma

9 | BE793530 601590016F1 NIH_MGC_7

10 | AL157542 DKFZp761D0816_x1 761 (

11 | BI770566 603060362F1 NIH_MGC_12

12 | AK013244 Mus musculus 10, 11 da

13 | AK013244 Mus musculus 10, 11 da

14 | BI910270 6030603493F1 NIH_MGC_12

15 | BF785386 602111728F1 NIH_MGC_12

16 | BF785386 602111728F1 NIH_MGC_12

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BG244406 602256535F1 NCI_CGAP_S
BE293685 601186941F2 NIH_MGC_15
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BE293685 601987474031F1 NIH_MGC_15
BE293685 6094474741 NIH_MGC_15
BE293685 60943041F1 NIH_MGC_14
BI140987 602962839F1 NCI_CGAP_BE250036 60943041F1 NIH_MGC_14
BI1457116 603185360F1 NIH_MGC_14
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BG831301 602766132F1 NIH_MGC_16
BG824757 602718745F1 NIH_MGC_15
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BE647090 UI-M-BH1-alx-e-10-0-UI
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BI764428 603050701F1 NIH_MGC_11
BM111403 daj86a10.y1 NICHD XGC
     53 za50h02.x1 Xenopus EST
53 TCBAP1E12081 Pediatrid
57 602511594F1 NIH_MGC_16
71 602329448F1 NIH_MGC_91
95 7n88c09.x1 NCI_CGAP_OV
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gb_est2:BM193252
gb_est2:BJ060637
gb_est2:BF569393
gb_est2:BE378839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
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Mammalia; Eutheria;
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5 (bases 1 to 1949)
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha
                                                                                                                                                                          Hayashizaki,Y
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BJ060637 BJ060637 NIBB Mochi
BF569393 602185659F1 NIH_MGC
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Tsurumi-ku, Yokohama,

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alignment_block:
US-09-155-327E-9 x AK015644
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                                                       232 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 281
                                                                                                                                 182 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 231
                                                                                                                                                                                                           132 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 181
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                       34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                       17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                                                 1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   632 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          582 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
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           Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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polyA_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2000) voshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) voshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research Group, RIKEN Gemomic Sciences Center (GSC), Exploration Research Group, RIKEN Gemomic Foliatory for Cohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9212, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="lung"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="1200009L24"
     /note="putative"
3487
                                                                                                                                                                                                                                                                                                                 data source:MGD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                               /note="Bcl2-like
                                                                                                                                                                                                                                                                                                                                                                    /gene="Bc1212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3487
                                                                                                                                                                                                                                                                                                                       source key:MGI:108052, evidence:ISS
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-155-327E-9 x AK004680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AK004680 from: 1
                                                                                                              seq_documentation_block:
                                                                                                                                                                 seq_name: gb_est2:BE793530
                                                                                           DEFINITION
SOURCE
                  KEYWORDS
                                                        ACCESSION
                                     VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 GGGAAGGCCCAGCCGACCGACCAAGCCATGCGGGCTGCTGGA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             459 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
|||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 oLeuValGlyGlnValGlnAspTrpMetValAlaIaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     509 GTCTTTGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AspGluPhcGluThrArgPheArgArgThrPhcSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 euAlaAspTrpIleHiaSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        559 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                  659 TACGGGGACGGGCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 708
                                                                                                                                                                                                                                                                                                                                                                                                  151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                    184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                      709 GCCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGGCCCTGG 758
                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 658
                                                                                                                                                                                                                                                                                                                           pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                             TAACTGTAGGGGCCTTTTTTGCTAGCAAG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 1006.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                LUJU DP MRNA linear EST 20-SEP-2000 601590016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5', mRNA secuence
                                       BE793530.1 GI:10214832
                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 99.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 3487
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ORGANISM

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alignment_block:
US-09-155-327E-9 x BE793530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 98.947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
344 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                             294 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 343
                                                                                                                                                                                                                                                                                          244 GGGAGGGCCCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 293
                                                                                                                                                                                                                                                                                                                                                                                       194 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 193
                                                                                                                            67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                 17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: LLCM800 row: p column: 04
High quality sequence start: 5
High quality sequence stop: 709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM800 row: p column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1030)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"organ: lung; vector: poTB7; Site_1: XhoI, Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       945.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:3944307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 95.789
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alignment_scores:
                                                                                                           ORIGIN
                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est1:AL157542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 ValThrValGlyAlaPhe 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         694 GTAACTGTAGGGGCCTTT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu. 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               594 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGGAGGGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 TGGCTGACTGGATCCACAGCAGTGGGGGGTTGGGGGGGAGTTCACAGCTCTA 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 euAlaAspTrpI1eHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                      Quality:
                                                                                                                                                                                                                                                                                                                        This clone (DKFZP761D0816) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140: Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cano Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                            No sl sequence available
                                                                                                                                                                                                                                                                                                                                                                                                                                German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                    Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S. EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Am Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 804)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKFZp761D0816_r1 761 (synonym: PDKFZp761D0816 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL157542.1 GI:7057943
                                                                                                                           150 a
                                                                                     /lab_host="pH10B"
/lab_host="pH10B"
/note="Vector: pSport1; Site_1: Not1; Site_2: SalI"
a 217 c 294 g 142 t 1 others
943.00
                                                                                                                                                                                /clone="DKF2p761D0816"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                             . 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 bp mRNA IIIICHI - CONA clone
                                                                                                                                                                                                                                                                                                                                                       Heubnerweg 6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      German Cancer
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Percent Similarity:

99.482

Percent Identity: 97.927

Ratio:

alignment\_block: US-09-155-327E-9 x AL157542

Align seg 1/1 to: AL157542 from: 1 to: 804

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seq_name: gb_est2:BI770566
                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                            ACCESSION
                                                  COMMENT
                                                                                                                                 REFERENCE
                                                                                                                                                                                             ORGANISM
                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGCTCTGGTGGCAGACTT 183
                                                                      JOURNAL
                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 GTCTTTGGGGCTGCACTGTGTGCNGAGAGTGTCAACAAGGAGATGGAACC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        384 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCCCTTGTAGCCTTCTTT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        633 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACT.GGGGCCCCTGG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                          682 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGGGGACGGGCC.CTGGAGGAGGCGCGCGTCTGCGGGAAGGGGAACTG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGGGGAGTTCACAGCTCTA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                    603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5',
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 697)
                                                  Contact: Robert Strausberg, Ph.D.
                                                                    National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                           NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                          BI770566.1 GI:15762144
                                                                                                                                                                                                                                                                                                    mRNA sequence.
Email: cgapDS 1 email: Life Technologies,
                              cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                  697 bp
                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                       linear
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alignment_block:
US-09-155-327E-9 x BI770566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: BI770566 from: 1 to: 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                              245 GGGAGGGCCCAGCAGCTGACCCGCTGCACCCAAGCCATGCGGGCAGCTGGA
                                            445 GTCTTTGGGGCTGCACTGTGTTGCTGAGAGTGTCAACAAGGAGATGGAAC 494
                                                                                                                                                         101 ValPheGlyAlaAlaLeuCys.AlaGluSerValAsnLysGluMetGluP 117
                                                                                                                                                                                                                       395 ATGAACTTTTTCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 lyGluGlyproAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
133 gLeuAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaL 150
                                                                                                                                                                                                                                            84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                        67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence start: 21
High quality sequence stop: 695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM11526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="organ: pooled lung and spleen; Vector: pCMV-SPORT6; /note="organ: pool of 24 week female lung, 16 week female anonymous pool of 24 week female lung, 16 week female spleens. Library is oligo-drespleen, and 20-22 week male spleens. Library is oligo-drespleen and directionally cloned (BooRV site is destroyed primed and directionally cloned (BooRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size upon cloning in sommalized and enriched for range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.835
97.326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5209862"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 nTrpAla.SerValArgThrVal.LeuThrGlyAlaValAlaLeuGlyAl 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            595 TATACGGGGGACGGGGCCCTGGAGGAGGCGCGGCGTCTGCGGGAGGGGAA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 euTyr.GlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAs 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 405, 685-690 (2001)

5 (bases 1 to 854)
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kuto, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer in 111 1757-1771
                                                                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muzamatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                            FANTOM Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA, clone_lib:RIEN full-length enriched mouse cDNA library
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                      (sites)
RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 (11), 1757-1771 (2000)
                                                 Quackenbush, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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REFERENCE

MEDLINE TITLE JOURNAL

PUBMED

AUTHORS

AUTHORS

TITLE

SOURCE VERSION

KEYWORDS

REFERENCE

JOURNAL

TITLE AUTHORS REFERENCE

MEDLINE JOURNAL TITLE

PUBMED

REFERENCE

MEDLINE JOURNAL

PUBMED

AUTHORS

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Align seg 1/1 to: AK013244 from: 1 to: 854
                                                                                                                                                                                                                                                                                                                     US-09-155-327E-9 x AK013244
246 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                     196 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 245
                             17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                            1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5] GAAGAGAAGAGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3/], CDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Host: SOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with XhoI and SstI. Cloning sites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAGAGAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax:81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAB28740.1"
/protein_id="BAB28740.1"
/db_xref="GI:12850488"
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/translation="MATPASTPDLAAQLHVTPGSAQQRFTQVSDELFQGGPWGRLVAFFVF
                                                                                                                                                                                                                                                                                                                                                                                                             5.182
98.667
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LHGKIGPLMGGWGCAGRG"
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196. .732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Bc1212"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="2810435A13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 96.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 days embryo"
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seq_name: gb_est2:BI910270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 GCTACACGTGACCCCAGGCTCAGCCAGCAACGCTTCACCCAGGTTTCCG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 eualaaspTrpIleHisSerSerGlyGlyTrpalaGluPheThralaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 spGluLeupheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603069493F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI910270.1 GI:16173653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: LLAM11548 row: j column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at:
                       /note="Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV /note="Vector: PCMV-SPORT6; Site_2: NotI] of the conting of the continuous of the con
                                                                                                                                                                                                                                                                                /clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:5218294"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
(Invitrogen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 643
       Research Genetics tracking code 027. Note:
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                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS BF785386
                                                                                                                                                                                                                                                                                                  seq_name: gb_est2:BF785386
                                                                                                                                                                                             ACCESSION
                                                                                                                                                                             VERSION
COMMENT
                                                                      REFERENCE
                                                                                                                                          SOURCE
                                                                                                                                                           KEYWORDS
                                                                                                                        ORGANISM
                                     TITLE
                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                               117 roLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       490 CACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                         587 CAAAGCTCGAGTCAGGGAGATGGAGGAAGAAGCTGAGAAGCTAAAGGAG 635
                                                                                                                                                                                                                                                                                                                                                                          150 uTyrGly......AspGlyAlaLeuGluGluAlaArgArgLeuArgGlu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGCATGGAAC 489
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 815)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                  602111728F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
                                                                                                                                                               EST
                                                                                                                                                                               BF785386.1 GI:12090422
Contact: Robert Strausberg, Ph.D
                                                                                                                                                house mouse.
                                                                                                                                                                                                                    , mRNA sequence.
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184 c 216 g 114 t
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                                                                                                                                                                                                                                                                 mRNA
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alignment_block:
US-09-155-327E-9 x BF785386
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                   141 erGlyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGlu 157
                                                                                                               124 pTrpMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSers 141
                                                                                                                                                                                 298 GCTGAGAGTGTCAACAAAGAAATGGAGCCTTG.GTGGGACAAGTGCAGGA 346
                                                                                                                                                                                                            108 AlaGluServalAsnLysGluMetGluProLeuValGlyGlnValGlnAs 124
                                                                                                                                                                                                                                                                          251 CTAACTGGGGCCGTCTTGTGGCATTCTTGTCTTGGGGC...TGCCTGTGT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 CGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTT.GAGACCCGTTTC 150
                                                                                                                                                                                                                                                                                                        91 roAsnTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCys 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 ArgArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySe 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 roLeuHisGlnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPhe 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 GAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGACC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 nLysGlyTyrvalCysGlyAlaGlyProGlyGluGlyProAlaAlaAspp 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 ProAspThrArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGl 24
GTGGGGGCTGGGAGTTCACAGCTCTATACGGGGACGGGCCCCTGGAG
                                                                                        TTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: LLAM9853 row: h column: High quality sequence start: 3 High quality sequence stop: 650.
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
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/Clone=lib="NCI_CGAP_Kid14"
/Clone=lib="NCI_CGAP_Kid14"
//lab_host="DH10B (T1 phage-resistant)"
/note="organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. | "
a 212 c 296 g 141 t
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alignment_block:
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                                                                                                                                                                                                                                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est2:BG298789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                      99 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 GACGGGGGCCCTGGCACT.GGGGCCCTGGTAACTGTAGGGGCCCTTTTTGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 TAGCACGT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 laserLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 uThrGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447 GAGGCACGGGT.CTGCGGGAGGGGAACGG.GCATCAGTGAGGACAGTGCT 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GluAlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLe 174
                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10394 row: e column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 792)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG298789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG298789.1 GI:13063794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 a
                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:4511215"
/clone="IMAGE:4511215"
/clone="IMAGE:4511215"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                             739.00
5.097
99.315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                        Percent Identity: 98.630
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seq_name: gb_est1:AW258810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 540) 1 (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW258810 540 bp mRNA linear EST 23-L
um74802.yl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:2300906 5' similar to SW:BCLW_MOUSE p70345 APOPTOSIS
REGULATOR BCL-W. [2] SW:BCLW_MOUSE;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW258810.1 GI:6631791
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/WashU-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                   seq primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                quality sequence stop: 465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouseest@watson.wustl.edu
                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:2300906"
/clone_lib="Sugano mouse kidney mkia"
/lab_host="DH10B"
                                                                    /sex="female"
                                                                                                                                                                                                                  /strain="C57BL"
                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                              _stage="adult"
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                                                                                                                                                                                                                          DEFINITION
                                          SOURCE
                                                                            KEYWORDS
                                                                                                              VERSION
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US-09-155-327E-9 x AW258810
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                                        seq_documentation_block:
                                                                        seq_name: gb_est2:BI764428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 GGGAAGGCCCAGCCGCCGACCCGACCAAGCCATGCGGGCTGCTGGA 261
                                                                                                                                                                                                                                                                                                                                                                         312 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                        17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                          412 GTCTATGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                        101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                         362 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                         462 TTTGGTGGGACAAGTGCATGATTGGATGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                          67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                           512 TGGCTGACTGGATCACAGCAGTGGGG 537
                                                                                                                                         134 euAlaAspTrpIleHisSerSerGly 142
                                                                                                                                                                                                                                                                                                                             84 spGluLeupheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                        oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
            603050701F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5',
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mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721.00
5.150
98.592
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                                          mRNA
                                            linear
                                             EST 25-SEP-2001
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BI764428.1 GI:15756006

EST.

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alignment_scores:
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Ratio: 5.143
Percent Similarity: 100.000
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389 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 438
                                                                                                       339 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 388
                                                                                                                                                                                                                                                                                                                          289 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                  189 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 188
                         84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                           67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                  51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11477 row: a column: 01
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Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 758)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=**Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:5190792"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .758
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alignment_block:
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
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                                                                                                169 TGTT.....CCAGAGCCTGCAGGACCAGCATCCTGTGCTTTGCATT 209
                                                                                                                                                                                             119 CGGGCTTTGGTGGAGGATTTTGTGCGGTACAAGTTATGCCAACGTAGTCT 168
210 CAGCTATGCGTGCTGCAGGGGATGAATTTGAGGAGCGATTCAGACAAGCA 259
                         11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
                                                                                                                                            27 rValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspProLeuHisG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 GTCTTTGGGGCTGCACTGTGTGCTGAAAGTGTTTCC 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.lln1.gov Seq primer: -40RP from Gibco High quality sequence stop: 386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM191403 601 bp mRNA linear EST 11-DEC-2001 daj86a10.y1 NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:5129754 5' similar to SW:AR1_XENLA Q91827 APOPTOSIS REGULATOR R1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            572.50
4.119
84.756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC)
) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5129754"
/clone_lib="NICHD XGC Lil"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 66.463
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DEFINITION vo21f08 r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1050567 5' similar to TR:E123735 E123735 R1 MRNA. ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 GGCGTATAGTTGCATTTTTTGTTTTTGGTGCCGCACTGTGTGCTGAGAGT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 GGAATGGATTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 GACATATCTGGAGACAAACCTGAGAGGCTGGATTCAGAGCAATGGAGGCT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 lalaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 GTCAACAAGGAGATGTCCCCTCTTCTGCCACGGATTCAAGACTGGATGGT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 ValAsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetVa 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 lyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSer 110
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                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i (bases 1 to 362)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich.N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA596919.1 GI:2412354
                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
                                                                                                                                                                                                                                                                                          primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                           quality sequence stop:
Location/Qualifiers
/note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cI
                                                                        /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
                                                                                                                         /clone="IMAGE:1050567"
                                                                                                                                                                        /strain="C3H"
                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                              /db_xref="taxon:10090"
                                              /lab_host="DH10B"
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est2:BF204905
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                                                                                                                                                          REFERENCE
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                                                                                                                                                                                                                       ORGANISM
                                                                                                                                         AUTHORS
                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 TITGAGACCCGTTTCCGCCGCACCTTCTCTGAACTGGCCGCTCAGCTACA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 TTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 yTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProGlyGluG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPheValG1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 PheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGlnLeuHi 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 lyproAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGlyAspGlu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 CTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 euPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePheValPhe 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                         601866718F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106836 5',
                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                      BF20490!
                                                                                                                    NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                   BF204905.1 GI:11098491
                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                               (bases 1 to 601)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               characteristic muscle proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3/]; double-stranded cDNA was ligated to Eco RI adaptors [AATTCCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rapidly, forming contractile myotubes and producing
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Percent Identity: 97.297
                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                EST 06-NOV-2000
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seq_name: gb_est2:BE508939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
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                                                                                                                                                                                                                  118 LeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgLe 134
                                                                                                                                                                                                                                                                                                                                                                                                   415 GAACTGTTTGCAAGGGGGCCCCAACTGGGGTTCGCTTGTAGCCTTCTTGG 464
                                                                                                         134 uAlaAsp.TrpIleHisSerSerGlyGly 143
                                                                                                                                                                                                                                                                                   465 TCTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCA
                                                                                                                                                                                                                                                                                                                  101 alPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPro 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 TCATGTGATCCCAGGCTCAGCCCAACAACGACTTCACCCAGGTCTCCGAT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 GGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGAGATGA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 GTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 CCAGCCTCGGCCCCAGACCACCACCGGCTCTGGTGGCAGACATTTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                     85 GluLeuPhe.GlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePheV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 .HisValThrProGlySerAlaGlnGlnArg.PheThrGlnValSerAsp 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 uPheGluThrArgPheArgArg.ThrPheSerAspLeuAlaAlaGlnLeu 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 GlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGlyAspGl 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 lyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProGlyGlu 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ProAlaSerThrProAsp...ThrArgAlaLeuValAlaAsp.PheValG 19
                                                       GGCTGATCTGGATCCAAAGAGAGTGGGGT 593
                                                                                                                                                                    CTGGTGGGACAAGTGCAGGAGTGGATGGTGGCTACTGTGAGACGCGGTCT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCM987 row: d column: 05 High quality sequence stop: 561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="rhabdomy/sarcoma"
/lab_bost="PH108 (phage-resistant)"
/lab_bost="PH108 (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Derkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
10 a 1/6 c 201 g 114 t
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4.199
90.476
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/clone="IMAGE:4106836"
/clone_lib="NIH_MGC_17"
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alignment_block:
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: BE508939 from: 1 to: 612
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LOCUS BE508939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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312 ACGATTTGCTGAAGTAGCAGGTAGCCTGTTCCAAGGAGGGGTGAATTNGG 361
                                                                                                    262 TTCAGTGAGATCTCCACACAGATCCACGTGACCCCCGGCACAGCATATGC
                                                                                                                                                                                                    212 CAGCTATGCGTGCTGCAGGGGATGAATTTGAGGAGCGATTCAGACAAGCA 261
                                                                                                                                                                                                                                                                                                      171 TGTT.....CCAGAGCCTGCAGGACCAGCATCCTGTGCTTTGCATT 211
                                                                                                                                                                                                                                                                                                                                                                                                              121 CGGGCTTTGGTGGAGGATTTTGTGCGGTACAAGTTATGCCAACGTAGTCT 170
                                        77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpG 94
                                                                                                                                                61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                                                                                                                                                                                               27 rValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspProLeuHisG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                         11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 439.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE508939 612 bp mRNA linear EST 07-AUG-20 dc14h09.yl NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:3397121 similar to SW:AR1_XENLA Q91827 APOPTOSIS REGULATOR R1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 612)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NICHD XGC Lil"
/lab_host="PHIOB (phage-resistant)"
/not="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) library."
128 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.915
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SIDS1/gogdata/geneseq/geneseqn-embl/NA1999.DAT:AAX25133 + 1002.00 1897.54 2.46
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/SIDS1/gogdata/geneseq/geneseqn-embl/NA1999.DAT:AAX25134 + 992.00 1874.61 4.56
/SIDS1/gogdata/geneseq/geneseqn-embl/NA1999.DAT:AAX25134 + 992.00 1874.61 4.56
/SIDS1/gogdata/geneseq/geneseqn-embl/NA1999.DAT:AAX25134 + 990.00 1874.61 4.56
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/SIDS1/gogdata/geneseq/geneseqn-embl/NA1999.DAT:AAX31818 + 420.50 792.70 8.36
/SIDS1/gogdata/geneseq/geneseqn-embl/NA1999.DAT:AAX31818 + 420.50 792.70 8.36
/SIDS1/gogdata/geneseq/geneseqn-embl/NA1999.DAT:AAX31818 + 420.50 772.35 1.26
/SIDS1/gogdata/geneseq/geneseqn-embl/NA1999.DAT:AAX33183 + 406.50 789.24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: Jun 6, 2002 2:37 PM
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Query: US-09-155-327E-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -0-/ggn2_1/USPTO_spool/US09155327/runat_06062002_084853_18524/app_query.fasta_1.508
-DB-N_Geneseq_032802 -QPMT=fastap -SUFFIX-p2n.rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPEXT=0.000 -GAPEXY=0.050 -XAPOP=10.000 -XAPEXT=0.500
-FGAPOP=4.500 -GAPEXT=7.000 -YAPAPOP=10.000 -YAPEXX=0.500
-DELEXT=7.000 -START=1 -MATRIX=blosum62
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pfs
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pfs
-NORM=0xt -HEAPSITE=500 -NINLEN=0 -MAXLEN=200000000
-NORM=0xt -HEAPSITE=500 -NINLEN=0 -MAXLEN=200000000
-USER=US09155327_@CGN1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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Database length: 858457221
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/SIDS1/gcjdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH45297 + /SIDS1/gcjdata/geneseq/geneseqn-emb1/NA2002.DAT:ABL32229 - /SIDS1/gcjdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF30926 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _p2n.model -DEV=xlh
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                         400.50
                                             753.30
729.16
                           749.13
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3.4e-36
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0 8.3e-36
1.2e-34
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8.3e-36
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4 5.3e-34
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1.1e-32
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1.5e-35
5.8e-36
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4.9e-34
4.9e-34
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1.2e-33
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                                                                            1.3e - 33
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                                                                              Align seg 1/1 to: AAX25133
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAH48169 + 400.06
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:AAT33694 + 396.50
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:AAQ81696 + 383.00
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV17638 + 371.50
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:ABA73433 - 369.50
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ID AAX25133 standard; DNA; 581 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX25133
                                                                                                                                                                                                                                                                                                                                                        The present sequence is the mouse bcl-w gene encoding Bcl-w protein CC (see AAY05531), a pro-survival member of the Bcl-2 family which is CC widely expressed and which is essential for spermatogenesis. The CC invention relates generally to a method of treatment and to an CC animal model for the identification of molecules and genetic Sequences useful for inducing or reducing fertility of male sequences useful for inducing or reducing fertility of male commands. Methods are provided for the treatment of infertility, or CC animals. Methods are provided for the treatment of infertility, or CC model carries a mutation is at least one allele of the human or CC murine bcl-w gene or in a gene associated with bcl-w. Such animals CC infertile, but possess no other major abnormalities as determined CC infertile, but possess no other major abnormalities as determined CC infertile, but possess no other major abnormalities as determined CC infertile, canimals including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in CC animals or which can induce infertility
                                                                                                                                                                                  alignment_scores:
                                alignment_block:
                                                                                       Percent Similarity: 100.000
US-09-155-327E-9 x AAX25133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        animal model; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09913710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 34; 52pp; English
                                                                                                                                                                                                                                                                          Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                       animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J, Cory S, Gibson L,
                                                                                                                              Quality: 1006.00
Ratio: 5.212
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                                                                    Opercent Identity: 99.482
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710.45
687.71
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3.2e-31
5.9e-30
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1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17

from: 1 to: 581

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seq_documentation_block:
IX
XX
AAV28333 standard; cD
AC AAV28333;
XX
DT 02-OCT-1998 (first e)
XX
DE Rat bcl-y gene.
XX
XX
SS; bcl-y; bcl-2; cel:
XX
SS; bcl-y; bcl-2; cel:
XX
COS Rattus sp.
XX
FH Key
FT CDS
FT CDS
FT CDS
FT CDS
FT CDS
FT CDS
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97US-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV28333
                                                                                                                                                                                                                                                              ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                                                                                                                                                                                                                                                      02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               AAV28333 standard; cDNA; 579 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 TACGGGGACGGGGCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 TGGCTGACTGGATCCACAGCAGTGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGlupheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GGGAAGGCCCAGCCGCCGACCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspGluPheGluThrargPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
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                                                                                                                                      /product= bcl-y
                                                                                                                                                             /*taq=
                                                                                                                                                                                               Location/Qualifiers
                                                                                                             "No stop codon given"
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alignment_block:
US-09-155-327E-9 x AAV28333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 100.000
134 eualaaspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu
                                                            351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT
                                                                                 117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                            301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                               101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                       251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                       201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                      151 GACGAGTTTGAGACCCGCCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GGGAAGGCCCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
                                                                                                                                                                                                                                               84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                              51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Column 13/14; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth e.g. cancers
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11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                              \verb|nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA|\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 1002.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0012201.
97US-0798897.
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Gaps:
                       150
                                                                                                                                                                                                                                                                                                           250
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX15945
CC generally multiple solerosis, movardial infarction, vitally induced cespecially multiple solerosis, may not be apparent. They may to selerosis - conditions where cells under go premature cell death, agono cells under go protein in thousand in the rapies to treat subjects suffering from: strokes, head trauma, cespecially multiple solerosis), myocardial infarction, vitally induced cespecially multiple solerosis, may or may not be apparent. They may also be cell death, aging, spinal cord injuries and amyotrophic lateral cespecially in this way to develop cell lines which remain viable in culture for cused in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, and extended period. In contrast, if they act as cell death stimulators, and subjects solerosis, conditions where cells under go premature cell death as a cell death.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 GGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX15945 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding the rat bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5883229-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-мау-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parasite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-NOV-1997;
                                                                                                                                                                                                                                                                                                             Disclosure; Columns 13-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                              Novel bcl-y homologues of the rat and human bcl-2 protein \, - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0012201.
97US-0798897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0978523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAX15945 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-155-327E-9 x AAX15945
seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX25132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GACGAGTTTGAGACCCGCCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 GCTACACGTGACCCCAGGCTCAGCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                     134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGlupheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                  351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                           117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                                                       451 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                               551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                    184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                          167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAAGGCCCAGCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                               TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                    GGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1002.00
Ratio: 5.192
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Percent Identity: 98.964
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seq\_documentation\_block:
ID AAX25132 standard; DNA; 581 BP.

05-JUL-1999 (first entry)

Human bcl-w gene

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alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the human bcl-w gene encoding Bcl-w protein (see AAY05530), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The circumstant in the control of the Bcl-2 family which is control of the preatment and to an animal series of the Bcl-2 family of the treatment of infertility, or control of the Bcl-2 family of the treatment of the Bcl-2 family of the treatment of the Bcl-2 family of the treatment of the Bcl-2 family o
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAX25132 from: 1 to: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-155-327E-9 x AAX25132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 997.00
Ratio: 5.166
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                              101 GGGAGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                             51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;
                                                                                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                            51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                         17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page 32; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                                                                                                                                          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                       1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAY05530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9913710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cory S, Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97AU-0009228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-AU00764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 98.446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Koentgen F, Print C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV28334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
growth e.g. cancers
    Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled
                                                                    WPI; 1998-446079/38
                                                                                               Guastella J;
                                                       P-PSDB; AAW61392
                                                                                                                                                                23-FEB-1996;
                                                                                                                      (COCE-) COCENSYS INC
                                                                                                                                                     11-FEB-1997;
                                                                                                                                                                                             11-FEB-1997;
                                                                                                                                                                                                                                                  US5789201-A.
                                                                                                                                                                                                                                                                                                                                                                           ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                              Human bcl-y gene
                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV28334;
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV28334 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501 GCCATCAGTGACGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                  96US-0012201.
97US-0798897.
                                                                                                                                                                                          97US-0798897
                                                                                                                                                                                                                                                                   /product= bcl-y
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350
        cell
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alignment\_block:

Percent Similarity:

US-09-155-327E-9 x AAX15946

alignment\_scores:

Quality: Ratio:

992.00 5.167 99.482

Percent Identity: 97.927 Length: Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

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XX CCCCCCCXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAV28334 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-155-327E-9 x AAV28334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression in vivo. Also, antisense const. where prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Column 15/16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
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                                                                                                                                                                                                                                                                            134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
                                                                                                                                                                               151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGAGITCGAGACCCGCITCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                   TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                   ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                        oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                     ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                       euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                       TACGGGGACGGGCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
                                                                                                          pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                alThrValGlyAlaPhePheAlaSerLys 193
                                                                         GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              992.00
5.167
99.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 97.927
579
                                                                                                                                                                                                                                                                                                                                400
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX15946
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CC specification also describes rat bcl-y protein (Rbol-y) and CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y CC proteins may be used to treat conditions associated with a disruption of CC proteins may be used to treat subjects suffering from: strokes, they may be CC lately in therapies to treat subjects suffering from: strokes, they may be CC especially multiple sclerosis, myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC ell death, aging, spinal cord injuries and amyotrophic lateral CC sclerosis- conditions where cells under go premature cell death as a CC result of triggers which may or may not be apparent. They may also be CC used in this way to develop cell lines which remain viable in culture for CC an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with CC Rbcl-y and Hbcl-y may be used to treat conditions associated with CC consecutions also clared with CC consecutions and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Raposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX15946 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding the human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5883229-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Columns 15-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel bcl-y homologues of the rat and human bcl-2 protein - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes human bcl-y protein (Hbcl-y).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW97392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0978523
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seq_documentation_block:
ID AAT96577 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAT96577
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W09735971-A1
                                                                                                                                                                                                                    Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                             diagnosis; degenerative disease; ss
                                                                                                                                                                                                                                                                                         Human bcl-w DNA.
                                                                                                                                                                                                                                                                                                                               22-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGGCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GGGAGGCCCAGCAGCTGACCCACTGCAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACGGGGACGGGGCCCTGGAGGAGGCGCGCGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euAlaAspTrpIleH1sSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA; 583 BP
                                           /product= bcl-w
                                                                                                            Location/Qualifiers
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alignment_block:
US-09-155-327E-9 x AAT96577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 100.000
301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                   101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                               251 ACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                               201 GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                 151 GATGAGTTCGAGACCCGCCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                                                                                                                                                                   101 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzhelmer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
                                                                                                     84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                       67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
                                                                                                                                                                                                                                                                            51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                   51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                         17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams JM, Cory S, Gibson LM, Holmgreen SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degenerative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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5.130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 97.409
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351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                           167
                                                                                                                                                                    451
                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                   401
                                                                                                                                                                                                                                                                                                                                                                          117
551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                         184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                      TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                       pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                        oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
|||||||||||||||||||||
                                                                                   GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                  TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
                                                                                              550
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seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX25134

seq\_documentation\_block:

AAX25134 standard; DNA; 583 BP.

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Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility; animal model; ss.
                                                                                                                                                                                                                           05-JUL-1999 (first entry)
                                                                                                                                                                                                                                     AAX25134;
                                                                                                                                                  16-SEP-1997;
                                                                                                                                                            16-SEP-1998;
                                                                                                                                                                                W09913710-A1
                                                                                                                                                                                         Homo sapiens
                                                                                                                                       (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                      25-MAR-1999
                                                                                                                               Adams J, Cory S, Gibson L,
                                                                                                                                                                                                                 bc1-w gene derivative
                                                                                                                                                   97AU-0009228.
                                                                                                                                                             98WO-AU00764.
                                                                                                                                Koentgen F,
                                                                                                                                Print C;
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inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce The present sequence is described as a derivative of the human bcl-w gene (see AAX25132), and encodes Bcl-w protein (see AAY05532), pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w  $\,$ Disclosure; Page 36; 52pp; English. P-PSDB; AAY05532. 1999-243890/20.

seq\_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAT96578

seq\_documentation\_block:

AAT96578 standard; DNA; 581 BP

X E X D X A X

(first entry)

Mouse bc1-w DNA 22-APR-1998

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Sox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAX25134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-155-327E-9 \times AAX25134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 583 BP; 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                     151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                                                                                                           117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                         301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 GCTGCATGTGACCCCAGGCTCAGCCAGCAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                        351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                        167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG
                              184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                             TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                           TGGTCGACTGGATCCACAGCAGTGGGGGGGTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                          euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                            TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G; 111 T; 0 other;
        579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.409
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alignment_scores:
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                                                                                                                                                                                                                                                                                                      US-09-155-327E-9 x AAT96578
                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzhelmer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w modulators
                                                                         101
                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 581 BP; 105 A; 164 C; 195
                                                                                                                                 51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCCTG
                                                                                                                                                   17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 50-51; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-489635/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-1997
                                                                                                                                                                                                1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW36048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09735971-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
diagnosis; degenerative disease; ss.
                                                                                                                                                                                                                    1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                  GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96AU-0008965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-AU00199
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5.142
98.446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= bcl-w
/note= "q"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibson LM,
                                                                                                                                                                                                                                                                                                                                     vaps: 0
Percent Identity: 96.373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holmgreen SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  G; 117 T; 0 other;
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX25135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                 An animal model exhibiting reduced levels protein associated with Bcl-w
                                                                                                   WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                               CDS
                                                                                       P-PSDB; AAY05533.
                                                                                                                                                 (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                               16-SEP-1997;
                                                                                                                                                                                                      16-SEP-1998;
                                                                                                                                                                                                                               25-MAR-1999.
                                                                                                                                                                                                                                                         WO9913710-A1.
                                                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                                                                                                                               animal model;
                                                                                                                                                                                                                                                                                                                                                                    Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                               Mouse bcl-w gene derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX25135 standard; DNA; 581 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 GGCATGAGTGAGCACAGTGGTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 ACGAACTTTTCCAAGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaphePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACGGGGACGGGCCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL
                                                                                                                          Cory S, Gibson L,
                                                                                                                                                                            97AU-0009228.
                                                                                                                                                                                                      98WO-AU00764
                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                          Koentgen F,
                                                          of
                                                                                                                         Print C;
                                                       a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400
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The present sequence is described as a derivative of the mouse

Disclosure; Page 38;

52pp; English.

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAX25135 from: 1 to: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-155-327E-9 x AAX25135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bcl-w gene (see AAX25133) and encodes Bcl-w protein (see AAY05533), pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries fertility, by modulating spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                  351
                                                                                                                                                                                                                                                                                                                                                                           117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGCCGACCCCAGCCTCAACCCCCAGACACACGCGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                    TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                              TGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                  TTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTC 400
                                                                                                                FACGGGGACGGGCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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5.142
98.446
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seq_documentation_block:
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                                                                                                                                                                                      alignment_scores:
                                                                       alignment_block:
                                                                                                    Percent Similarity: 100.000
                             Align seg 1/1 to: AAV41925
                                                         US-09-155-327E-9 x AAV41925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV41925 standard; cDNA; 1098 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunological disorder; autoimmune disease; anti-infectious agent;
                                                                                                                                                                                                               This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9831800-A2.
                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                   or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-414099/35.
P-PSDB; AAW59884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feng P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AUCK-) AUCKLAND UNISERVICES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                      Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other;
1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gentz RL, Krissansen GW,
                                                                                                                  Ratio:
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97US-0034204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Bcl-like (HAICH29) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                   756.00
                                                                                                                       5.250
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                                  from: 1 to: 1098
                                                                                                       Percent Identity: 97.917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ni J,
                                                                                                                                     Length:
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07-MAR-1997,
07-MAR-1997,
07-MAR-1997,
07-MAR-1997,
07-MAR-1997,
07-MAR-1997,
07-MAR-1997,
07-MAR-1997,
                                                                                                                                                                                                                                                                  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                   06-MAR-1998;
                                                                                                                                                                                               11-SEP-1998
                                                                                                                                                                                                                          W09839448-A2
                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                19-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein gene 120 clone HGBGZ64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV59630 standard; DNA; 1864 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProg 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspGluPheGluThrargPheArgArgThrPheScrAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGCTGACTGGATCCACAGCAGTGGGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCCGGC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
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                                                                                                                                                                                                                                                     sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
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97US-0038621
97US-0040161
97US-0040162
97US-0040333
97US-0040333
97US-0040334
97US-0040334
97US-0040334
97US-0040331
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    23-MAY 1997
24-AUG-1997
25-AUG-1997
27-AUG-1997
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23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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11-APR-1997;
11-APR-1997;
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11-APR-1997;
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11-APR-1997;
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                                                                                                                                                                97US-0048964.
97US-0048971.
97US-004910.
97US-0051926.
97US-0055274.
97US-0056630.
97US-0056631.
97US-0056636.
97US-0056636.
97US-0056636.
97US-0056636.
97US-005664.
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97US-0047615.
97US-0047617.
97US-0047618.
97US-0047632.
97US-0047633.
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970S-0043569

970S-0043576

970S-0043671

970S-0043671

970S-0043671

970S-0047500

970S-0047501

970S-0047501

970S-0047501

970S-0047581

970S-0047581

970S-0047582

970S-0047583

970S-0047584

970S-0047584

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970S-0047593

970S-0047593
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97US-0043313.
97US-0043314.
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alignment_scores:
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                                                                                                                                                                                                                            US-09-155-327E-9 x AAV59630
                                                                                                                                                                                                                                                                            Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                  Arcc 209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic rhe invention relates to 186 novel genes and their fragments (nucleic rhe invention sequences: AAV5951-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polynucleotides. Specific uses are described for each of the 186 the new polynucleotides. Specific uses are described for each of the 186 novel gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feng P,
Kyaw H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW74848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 353-354; 721pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-506364/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bednarik DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                          Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                           (see AAV59511 for described uses).
                                                                                                                              11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 60
                                                                                               17
                             34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                61
                                                                                                                                               1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a nucleic acid molecule designated Gene 120 the human cDNA clone HGBGZ64 (deposited as clone ATCC 97902 and
TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 110
                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0056893.
97US-0056894.
97US-0056903.
97US-0056908.
97US-0056910.
97US-0056910.
97US-0056911.
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97US-0057669.
97US-0057761.
97US-0058785.
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97US-0056887.
                                                                                                                                                                                                                                                                                                               756.00
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Soppet DR,
                                                                                                                                                                                                  from: 1 to: 1864
                                                                                                                                                                                                                                                                                  Percent Identity:
                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                     97.917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endress GA;
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinfiammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated gene SEQ ID NO: 201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL32228 standard; DNA; 6049 BP
The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200928-A2
                                                                                                                Claim 1; SEQ ID NO 201; 32pp + Sequence Listing; German
                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                       Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                    02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                 WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
                                                                                                                                                       cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCTGACTGGATCCACAGCAGTGGGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442
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leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel

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seq_documentation_block:
ID AAS00247 standard; DN
XX AC AAS00247;
XX
DT 31-MAY-2001 (first &
XX
DT 31-MAY-2001 (first &
XX
DE Bcl-X1-DTR apoptosis.
XX
KW Human; Bcl-X1-DTR; application;
KW diphtheria toxin recension to the secondary of the seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAS00247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-155-327E-9 x ABL32228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5401 TGGTTGATTGGATTTATAGTAGTGGGGGTTGG 5432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5351 ATTGGTGGGATAAGTGTAGGAGTGGATGGTGGTTTATTTGGAGACGTAGT 5400
                                                                                                                                                                                                        diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5151 GATGAGTTCGAGATTCGTTTTCGGCGTATTTTTTTTTTGATTTGGCGGTTTA 5200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5101 GGGAGGGTTTAGTAGTTGATTCGTTGTATTAAGTTATGCGGGTAGTTGGA 5150
                                                                                                 Chimeric - Homo sapiens
                                                                                                                                                                                          Huntington's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bcl-xl-DTR apoptosis-modifying fusion protein, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5051 TGTAGGTTATAAGTTGAGGTAGAAGGGTTATGTTTGTGGAGTTGGTTTCG 5100
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                                                                                                                                                                                                                                                                                                                                           Human; Bcl-xl-DTR; apoptosis; cancer; spinal muscular atrophy; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AASO0247 standard; DNA; 1236 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTTTTGGGGTTGTATTGTGTGTTGAGAGTGTTAATAAGGAGATGGAATT 5350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
             Corynebacterium diptheriae Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           438.00
3.744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 63.889
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alignment\_block:

Percent Similarity:

63.090 429.50

Percent Identity: 39,485

Quality: Ratio:

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apoptosis in a subject after transient ischaemic neuronal injury, apoptosis in a subject after transient ischaemic neuronal injury, especially spinal cord injury. The fusion protein may be used to treat various diseases and injury conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, spinal muscular atrophy, stroke episodes and unregulated cell growth as in tumours and various cancers. The apoptosis modifying fusion protein can be delivered effectively throughout the body and targeted to selective tissue and
                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the coding sequence of Bcl-Xl-DTR apoptosis-modifying fusion protein comprising human Bcl-Xl sequence fused via a short linker to diphtheria toxin receptor binding domain (DTR). The functional apoptosis-modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the target cell. The apoptosis-modifying fusion protein comprises at least two domains: the DTR domain, which targets the fusion protein to the target cell and the Bcl-XL domain, which modifies an apoptotic response of the target cell. The fusion protein is useful for modifying (inhibiting or enhancing) apoptosis in a target cell, such as neuron, lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyper-proliferative cell or an adipocyte. It is also useful for reducing another is a sentent sector of the content of the cell or an adipocyte. It is also useful for reducing
                 Sequence 1236 BP; 317 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 54-56; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAU00219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Youle RJ, Liu X, Collier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-2000; 2000WO-US22293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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/note= "Linker DNA, linking Bcl-xl to DTR'
778..1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Bcl-Xl gene from codon 1-233"
760...777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "DTR, diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Bc1-x1-DTR fusion protein"
/note= "DTR is diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "10x Histidine tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
291 C; 343 G; 285 T; 0 other;
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US-09-155-327E-9 x AAS00247

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W X E X E X E X X X
                                                                                                                                                                                                                                                         seq_documentation_block: ID AAF75960 standard; cDNA; 1742 BP.
                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF75960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 CGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGCAAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 GACAAGGAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AsnLysGluMetGluProLeuValGlyGlnValGlnAspTrpMetValAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 GCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 ArgAlaLeuValAlaAspPheValGlyTyrArgLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 r..... 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 CGGGAGCTGGTTGACTTTCTCTCTACAAGCTTTCCCAGAAAGGATA 125
Rat Bcl-xL; apoptosis inhibitor; programmed cell death inhibitor;
wild-type; antiapoptotic; cell death-associated disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                    Rat wild-type Bcl-xL cDNA.
                                                                                                                                          22-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....ProLeuHisGlnA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ......ValCysGlyAlaGlyPro 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 625
                                                                                                                                                                                                                                                                                                                                                                                                      CGTGGTTCTGCTGGGCTCACTCTTCAGTCGGAAAGCGTATTCTGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             yAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaSer 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: AAS00247 from: 1 to: 1236
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAF75960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a mutant rat Bcl-x protein and the cDNA encoding it. The mutant rat Bcl-x protein (Bcl-xFNK) has the substitutions Y22F, Q26N, and R165K relative to the wild-type Bcl-xL protein The invention also encompasses recombinant vectors and host cells comprising the modified nucleic acid sequence. The mutant Bcl-x protein is able to permeate the cell membrane, thus enhancing its ability to be taken up into a cell and to act as an inhibitor of apoptosis (programmed cell death). Bcl-xFNK and nucleic acids encoding apoptosis in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in remedies for diseases associated with cell death and it are useful in the cell in 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue transplant preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 43-45; 56pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB73303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-2000; 2000WO-JP05502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1742 BP; 377 A; 507 C; 477 G; 381 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in additives for maintaining the stability of transplanted cells and organs. The present sequence represents cDNA encoding wild-type rat Bc1-xL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 CAGCTGGAGTCAGTTTAGCGATGTCGAAGAGAACAGGACTGAAGCCCCAG 186
                                                                                                                                                                                                                                                                                                                                     187 AAGAAACTGAACCAGAAAGGGAGACCCCCAGTGCCATCAATGGCAACCCA 236
                                                                                                                                                                                                  237 TCCTGGCACCTGGCGGATAGCCCCGCGGTGAATGGAGCC...ACTGGCCA
                                                                      284 CAGCAGCAGTTTGGATGCGCGGGAGGTAATCCCCATGGCAGCAGTGAAGC
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44 lnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
                                                                                                                               uGlyProAlaAlaAsp......ProLeuHisG 44
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334 61	AAGCGCTGAGAGAGGCTGCGCGATGAGTTGAACTGCGGTACCGGAGAGACA PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl
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434	GAGCTTTGAACAGGTAGTGAATGAACTCTTTCGGGATGGGGTAAACTGGG
94	lyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAla
484	GTCGCATTGTGGCCTTCTTCTCTTTGGCGGGGCACTGTGCGTGGAAAGC
111	
534	GTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATTGCAAGTTGGATGGC
127	lAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyT
584	CACCTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGCCT
144	rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg
634	GGGACACTTTTGTGGATCTCTACGGGAACAATGCAGCAGCCGAGAGCCGG
161	:
684	AAAGGCCAGGAGCGTTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGC
175	rGlyAlaValAlaLeuGlyAlaLeu 183
734	TGGTGTAGTTCTGCTGGGCTCACTC

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OM of: US-09-155-327E-9 to: GenEmbl:*
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gb_pat:AX022531
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i AF096291 Rattus norvegicus BC1-
i U59747 Human BC1-w (bC1-w) mRNP
                                                                                                                                                                  i BD006625 A mutagenized rat bol
i U72350 Rattus norvegicus Bol-x
i M7054021 Sequence 6 from patent
AR118504 Sequence 1 from patent
AR124952 Sequence 3 from patent
AR144311 Sequence 3 from patent
AR172594 Sequence 6 from patent
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AJ001203 Sus scrofa mRNA for an
AF660226 Eukaryottic expression
X835/4 M.musculus bol-xL mRNA.
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1 051278 Mus musculus thrus Bol

1 026645 Gallus gallus bol-x (bo

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AF164517 Ovis aries Bcl-x long
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BC019307 Homo sapiens, clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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gb_ro:RNCBLXLS
gb_ro:RNU10579
gb_om:BTU92434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS MMU59746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_ro:MMU59746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pat:E23357
                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                            alignment_block:
                                                                                                                                                                                                                                                        Quality: 1006.00
Ratio: 5.212
Percent Similarity: 100.000
                                                                                                                                                                   Align seg 1/1 to: MMU59746
                                                                                                                                                                                                          US-09-155-327E-9 \times MMU59746
34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                  51 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                     17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                   Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival oncogene 13 (4), 665-675 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus Bcl-w (bcl-w) mRNA, complete cds. U59746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U59746.1 GI:1572494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, po Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cory, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96358615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 582)
                                                                                                                                                                                                                                                                                                                                                                                   107
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="promotes cell survival; Bcl-2 homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424.50
421.50
417.50
412.50
411.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           line="BaF3"
                                                                                                                                                                            from: 1 to: 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           626.58
631.76
634.41
627.67
615.78
                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 99.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        582 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5e-26
7.9e-27
5.7e-27
1.3e-26
6.2e-26
                                                                                                                                                                                                                                                                                   Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7372 | E23357 Virus vector system
2232 | x82537 R.norvegicus bcl-x g
764 | U10579 Rattus norvegicus Bcl
687 | U92434 Bos taurus bcl-2 mRNA
2228 | z11961 G.domesticus mRNA fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E23357 Virus vector system | x82537 R.norvegicus bcl-x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROD 29-SEP-1996
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_ro:AF030769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 GCCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 GCTACACGTGACCCCAGGCTCAGCCCAGCCTTCACCCAGGTTTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 GGGAAGGCCCAGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 350
                                                                                                                                                                                                                                                                                                               University,
                                                                                                                                                                                                                                                                                                                           Submitted (21-0CT-1997) Center for Molecular Medicine,
                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                 Ross, A.J. and MacGregor, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ross, A.J., Waymire, K.G., Moss, J.E., Parlow, A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus BCL-W (Bcl-w) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bcl-w is required for testis homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MacGregor, G.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF030769.1 GI:2623249
                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 3476)
                           /number=1
                                             /gene="Bcl-w"
                                                                                             /gene="Bcl-w"
                                                                                                                                        /map="
                                                                                                                                                                 /chromosome="14"
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                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                         . 82
                                                                                                                                                                                                                                                                                                          1462 Clifton Road, Atlanta, GA 30322, USA
                                                                                                                                           19.5 cm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3476 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Russell, L.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROD 16-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AF030769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-155-327E-9 x AF030769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 100.000
579 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 628
                         134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                       529
                                                                                                                                        117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                       479
                                                                                                                                                                                                                                                                                      429 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                     101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                   379 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA
                                                                                                                                                                                                                                                                                                               84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                 67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                           GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                          TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 1006.00
Ratio: 5.212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="mRNA destabilization element" 3428. 3441 /gene_"Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=4
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GAALCAESVNKEMEPLVGQVQDwMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RUREGGWWASVRTVLTGAVALGALVTVCAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=2
171. .610
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179. .760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3356. .3364
/gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="BCL-W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Bcl-w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .3476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to: 3476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 99.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        991 g
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451

401

REFERENCE AUTHORS

TITLE AUTHORS

JOURNAL

REFERENCE

SOURCE KEYWORDS VERSION DEFINITION ACCESSION

ORGANISM

FEATURES

source

gene

578

528

JOURNAL TITLE

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LOCUS AR020779
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-155-327E-9 x AR020779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AR020779 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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201 GCTACACGTGACCCCAGGCTCAGCCAGCACGCTTCACCCAGGTTTCCG 250
                                                                                                                                                                        51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                       17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                   51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                        34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                        251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                      84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                         67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                 1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                 1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                 GGGAAGGCCCAGCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5/9 Dp
Sequence 1 from patent US 5789201.
AR020779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes coding for bcl-y a bcl-2 homologue patent: US 5789201-A 1 04-AUG-1998; Location/Qualifiers
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Guastella,J.
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Ratio: 5.192
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157 c 198 q
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seq_name: gb_ro:AF096291
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 TGGCTGACTGGATCCACAGCAGTGGGGGGTGGGCGGAGTTCACAGCTCTA 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF096291.1 GI:3747129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hamner,S., Skoglosa,Y. and Lindholm,D.
Differential expression of bcl-w and bcl-x messenger RNA in the
developing and adult rat nervous system
Neuroscience 91 (2), 673-684 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-OCT-1998) Developmental News University, Box 587, BMC, Uppsala 751 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamner,S., Skoglosa,Y. and Lindholm,D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus
                                              Quality: 1002.00
Ratio: 5.192
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                                                                                                                                                                                                                                                111 a
                                                                                                                                                                                                                                            PROTEIN_IG="AAC64200.1"
/protein_IG="AAC64200.1"
/protein_IG="AAC64200.1"
/db_xref="GI:3747130"
/db_xref="GI:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Sprague-Dawley'
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="Bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="postnatal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="brain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Bcl-2 family member"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="bcl-w"
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                 Percent Identity: 98.964
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alignment\_block:

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ORGANISM
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LOCUS HSU59747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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              Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)
Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival 96358615
                                                                                                                                                                                                                                                     Human Bcl-w (bcl-w) mRNA, complete cds. U59747
                                                                                                                                                                           Homo sapiens
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Percent Similarity: 100.000
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134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
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                                                                                                                                         351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                             117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                     301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                      101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 ACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cory, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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/product="Bc1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   997.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="14q11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 98.446
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151

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seq_documentation_block:
LOCUS BC021198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 TGGCTGACTGGATCCACAGCAGTGGGGGGGTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC021198 1437 bp mRNA linear PRI 22-JAN-
Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; web stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC021198.1 GI:18203706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Brooks, S., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 15 Row: k Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14574571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1437)
                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="LocusID:599"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                         /tissue_type="Lung, small cell carcinoma"
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="MGC:10675 IMAGE:3944307"
/product="BCL2-like 2"
/protein_id="AAH21198.1"
/db_xref="GI:18203707"
                                                                                                                                       /note="Vector: pOTB7"
                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRI 22-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 5.166 Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-155-327E-9 \times BC021198
                                                                                                                                                                                            seq_name: gb_pr:D87461
                                                                                                                                          seq_documentation_block:
                                                                                      DEFINITION
                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576
                                                                                                                                                                                                                                                                                                                                                                                                                                      167
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                                                                                   Human mRNA for KIAA0271 gene, complete cds.
                                                             D87461
                              D87461.1 GI:1944417
                                                                                                                     D87461
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COMMENT

REMARK

FEATURES

3542 bp

mRNA

linear

PRI 06-OCT-2001

ACCESSION

SOURCE KEYWORDS VERSION

REFERENCE

TITLE

JOURNAL AUTHORS

```
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a 343 c 509 g 282 t
                                                                     997.00
owaps: 0
Percent Identity: 98.446
                                                                             Length:
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Align seg 1/1 to: BC021198 from: 1 to: 1437 176 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 225 276 GGGAGGGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 325 426 ATGAACTITTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 475 134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150 476 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 525 101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50 151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167 526 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134 17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100 1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17 184 alThrValGlyAlaPhePheAlaSerLys 193 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184 675 575

KEYWORDS

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-155-327E-9 x D87461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 5.166
Percent Similarity: 100.000
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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277
                                                                                                                                                                                     227 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                            177 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 226
                                                                                                                        34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                             17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                    1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                           GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced by analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; (bases 1 to 3542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Protein_id="BAA19666.1"
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GAALCAESVNKEMEPLVGQVQEMYVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLRECKWASVRTVLTGAVALGALYTVGAFFASK"
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177 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="KIAA0271"
177. .758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to human transforming protein bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       997.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="KIAA0271"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_line="KG-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="HA6752"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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LOCUS AR020780
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                                 51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                        17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     727 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 755
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                                                                                                           1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 50
                                                                                                                                              1 MetalaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
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154 c 208 g
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150

51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67

Thu Jun

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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified.
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Percent Similarity: 100.000
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                                             REFERENCE
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                                                                                                                                  583 bp
Sequence 6 from Patent W09735971.
AX030817
1 (bases 1 to 583)
Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
                                                                                                                        AX030817.1 GI:10278311
                                                             unclassified
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501 GCCATCAGTGAGGACAGTGCTGACGGGGCCCGTGGCACTGGGGGCCCCTGG 550
                           167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                            451 TACGGGGACGGGCCCTGGAGGAGGCGCGCCGTCTGCGGGAAGGGGAACTG
                                                                                                                     151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                            134 eualaaspTrpIleHisSerSerGlyGlyTrpAlaGluPheThralaLeu 150
                                                                                                                                                                                                                                                                                                                                                                           301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                                                    101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 ACGAACTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                     ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                                                                                                                                           OLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nLeuH1sValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspGluPheGluThrargPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGAGGGCCCAGCAGCTGACCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
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ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZANNE (AU); GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
LOCATION/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
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GAALCAESVNKEMEPLVGQVQEMWVAYLETRLVDWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVVAAFFASK"
a 157 c 210 g 111 t
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alignment_block:
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SOURCE
ORGANISM
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ACCESSION
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251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
                                                                           201 GCTACACGTGACCCCAGGCTCAGCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                         151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                      101 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                   84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                             51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                         34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                  51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG 100
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                                                                                                                                                                                                                                                                                                                                                                                               1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaThrProAlaSerThrProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 alThrValGlyAlaPhePheAlaSerLys 193
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Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes
patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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Percent Identity: 96.373
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seq_name: gb_pat:AX030819
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ORIGIN
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                                                                        Align seg 1/1 to: AX030819
                                                                                                              US-09-155-327E-9 x AX030819
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oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
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A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
apoptosis-controlling genes
Patent: WO 9735971-A 8 02-OCT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZANNE (AU);
GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
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5.142
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                                                 COMMENT
                                                                                                                                                                                      REFERENCE
                                                                                                                                          AUTHORS
TITLE
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                                                                                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 ACGAACTTTTCCAAGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501 GGCATGAGTGAGCACAGTGGTGACGGGGGCCCTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 alThrvalGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGGGGACGGGCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCTGACTGGATCCACAGCAGTGGCGGCTGGGCGGACTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS0000B 196292 bp DNA linear PRI 22-MAY-
Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                       Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguena Levy, M., Bckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196292)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
                        Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                     Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL049829.4 GI:8217859
Center: Genoscope / Centre National de Sequencage
                                                                                                                                          Direct Submission
                                                                                                                                                                   Genoscope
                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                      (bases 1 to 196292)
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                                                                                                                                                                                                                                                                                                                  Artiguenave, F.,
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Overall quality chart :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end): R-244E17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap; version 2.0 Quality coverage: 7.94x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC-AL132855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: GS
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                                          128419. 128543
/note="matching EMBL:R87257
                     dbsts:sts18321
                                        RHdb:RH53698
                                                                                                             dbSTS:STS25817
                                                                                                                                  RHdb: RH53520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identified using the e-PCR software (G. Schuler)" 82164. 82299 /notee-"matching EMBL:H79035 RHdb:RH78773
                                                                                                                                                                                                                            RHdb:RH47139
                                                                                                                                                                                                                                                                                                    dbSTS:STS45044
                                                                                                                                                                                                                                                                                                                                                                                              dbSTS:STS52191
                                                                                   Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                   Identified using the e-PCR software (G. 128387. .128525
                                                                                                                                                                                                                                        /note="matching EMBL:D11677
                                                                                                                                                                                                                                                                 107996. .108181
                                                                                                                                                                                                                                                                                                                                                                                                                  RHdb:RH75103
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                                                                                                                                              note="matching EMBL:H22648"
                                                                                                                                                                                                                                                                               Identified using the e-PCR software
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                                                                                                                                                                                                                                                                                                                                                             107758.
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/note="matching EMBL:AA167748
RHdb:RH98727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identified using the e-PCR software
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RHdb:RH102162
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30433. .80566
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                                                                                                                                                                                   Schuler) "
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US-09-155-327E-9 x CNS0000B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: CNS0000B from: 1 to: 196292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                      90026 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 90075
                                                                                                                              89976 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 90025
                                                                                                                                                                                                                                                                               89876 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 89925
                                                                                                                                                                                                       89926 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 89975
                                                                                                                                                                                                                                                                                                                                                       89826 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 89875
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaphePhe 100
                                                                        67 nLeuHisValThrProGlySerAlaGlnGlnArgPhgThrGlnValSerA 84
                                                                                                                                                  51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                            34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                    17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
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RHdb:RH28671
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138462. .138738
//note="matching EMBL:R59134"
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90126 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGGGAACC 90175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                         90926 TGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTG
                                                                                                                                                                             90826 GATATCCCTTCTCCTTCTTCTCTCCTGCTTCCCTTCTCTCCCACAGGC 90875
                                                                                                                                                                                                                                                                                                                                                        90776 GATGGAACTGGAACTCTTCCTCTCTCTCTCTCCACTCTTTCCTCTCCT 90825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 ...... 144
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162 euArgGluGlyAsnTrpAlaSerValArgThrValLeuThrGlyAlaVal 178
                                                                                                                                                                                                                   146 .GlupheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArgL 162
                                                                                                                                                                                                                                                                                                         145 ......Ala 145
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JOURNAL
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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                                                                                                       FEATURES
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                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Ho,S.-L., Idol,J., Karlins,E., Lee-Lin,S.-Q., Legaspi,R., Lim,M.,
Maduro,Q.L., Maduro,V.B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.
NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC079885.2 GI:11120768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Nov 8, 2000 this sequence version replaced gi:10179358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                      * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 151212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 147800 bases at least 040 consensus quality: 148726 bases at least 030 consensus quality: 148333 bases at least 020 consensus quality: 149333 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 14500; agarose fp
Insert size: 150812; sum-of-contigs
Quality coverage: 11.76x in Q20 bases; agarose-fp
Quality coverage: 11.30x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: rk
Center clone name: 246F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                    20441
20541
41010
41110
65553
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                                                                                                                                                                                          65653
/strain="Brown Norway"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- Genome Center
                                                      /organism="Rattus norvegicus"
                                                                                                          Location/Qualifiers
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    Summary Statistics

                                                                                                                                    110365: gap of unknown length
110365: contig of 44713 bp in length
110465: gap of unknown length
151212: contig of 40747 bp in length
                                                                                                                                                                                                                                           41109: gap of unknown length 65552: contig of 24443 bp in
                                                                                                                                                                                                                                                                                               20440: contig of 20440 bp in length 20540: gap of unknown length 41009: contig of 20469 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151212 bp
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alignment_block:
US-09-155-327E-9 x AC079885
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43370 a 30838 c 31177 g 45417 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 86.528
                                                                        74915 TGGCTGACTGGATCCACAACAATGGGGGCTGGGTGGAGTTCACAGCTCTA 74964
                                                                                                                                                                                                                                                                      74865
                                                                                                                                                                                                                                                                                                                                                                                                                                     74765 ACGAACTTTTCCAAGGGGCCCCAACTAGGCCCATCTTGTGACACTTCTTT 74814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74715 GCTACATGTGATGCCAGGCTCAGCCCAACAATGCTTCACCCAGGTTTCCA 74764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74665 GACAAGTTAGAGACCCACTTCCAGCACACCTTCTCTGACCTGGCCACTCA 74714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74615 GGGAAGGCCCAACAGCCAACCTGATACACCAAGCCATGTGGGCTGCTGGA 74664
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                        167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                              151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                          134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                       101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                                                                                                oLeuValGlyGlnValGlnAspTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                        ATTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCCAGAGACACGCC 74914
                                                                                                                                                                                                                                                                                                                                                 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAGAAAAATAGAGCC 74864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
Quality:
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4.036
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110466. .151212
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65653. .110365
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clone_end:SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_end:T7
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75015 GGCATCAGTGAGGACAATACTGACTGGGGCTGTGACACTGGGGACCCTGA 75064
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                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Dietrich,N.L., Gupta,J., Ho,S.-L.,
Idol,J., Lee-Lin,S.-Q., Legaspi,R., Lim,M., Maduro,Q.L.,
Maduro,V.B., Mastrian,S.D., McCloskey,J.C., McDowell,J.,
Pearson,R., Prasad,A., Snyder,B., Stantripop,S., Thomas,J.W.,
Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tran,J.T., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.
NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus chromosome 4 clone RP31-103L21 st
Norway, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC084240.1 GI:10864175
                                                                                                                                                                                                                             be preserved.
                                                                                                                                                                                                                                                     as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 181282)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 181282)
                                                                5431
5531
39504
39604
85793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 13800; agarose-fp
Insert size: 160000; pulse-field-gel
Insert size: 160000; pulse-field-gel
Insert size: 160982; sum-of-contigs
Quality coverage: 15.02x in 020 bases; agarose-fp
Quality coverage: 12.95x in 020 bases; pulse-field-gel
Quality coverage: 11.45x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.99319 Consensus quality: 179798 bases at least 040 Consensus quality: 180132 bases at least 030 Consensus quality: 180134 bases at least 030 Consensus quality: 180274 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: rl
Center clone name: 103L21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Summary Statistics
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Location/Qualifiers
            5430: contig of 5430 bp in length
5530: gap of unknown length
39503: contig of 33973 bp in length
39603: gap of unknown length
85792: contig of 46189 bp in length
85892: gap of unknown length
181282: contig of 95390 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Center
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4 clone RP31-103L21 strain Brown
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BASE COUNT
ORIGIN
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US-09-155-327E-9 x AC084240
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Percent Similarity: 86.528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AC084240 from: 1 to: 181282
                                                                                                                                                                                                                                              49782 ATGGCAACCCCAACCTCAATCCCAGACACATGGGCTCTAATGGTTGA... 49828
                                   49989 ACGAACTTTTCCAAGGGGGCCCCAACTAGGGCCATCTTGTGACATTCTTT 50038
                                                                                                                                                                                                                                                                                                  misc_feature
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151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                 17 eValGlyTyrArgLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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85893. 181282
/note="assembly_fragment"
3 36290 c 37296 g 56560 t
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39604. .85792
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clone_end:SP6
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/organism="Rattus norvegicus"
/strain="Brown Norway"
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/chromosome="4"
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4.036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP31-103L21"
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Sequence List:

Strd Orig ZSCOTE ESCOTE Len | DOCUMENTATION 7.3e-110 579 | Sequence | Se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                About: Results were produced by the GenCore software, version 4.5
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Query length: 193
Database: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database sequences: 383533
Database length: 122816752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search time (sec): 65.480000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1993-2000 Compugen Ltd
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/cgn2_6/ptodata/l/ina/PcTUS_COMB.seq:PCT-US94-07089-8 + 183.00 367.00 9.4e-13 /cgn2_6/ptodata/l/ina/SA_COMB.seq:US-08-471-058-6 + 176.00 340.26 2.9e-11 20 /cgn2_6/ptodata/l/ina/SB_COMB.seq:US-08-944-530-1 + 176.00 340.26 2.9e-11 20 /cgn2_6/ptodata/l/ina/SB_COMB.seq:US-08-471-057-6 + 176.00 340.26 2.9e-11 20 /cgn2_6/ptodata/l/ina/SA_COMB.seq:US-08-471-058-8 + 173.00 339.41 3.2e-11 11 /cgn2_6/ptodata/l/ina/SA_COMB.seq:US-08-471-058-8 + 173.00 339.41 3.2e-11 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-798-897-2
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                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-798-897-2 from: 1 to: 579
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                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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TITLE OF INVENTION: Homologue
NUMBER OF SEQUENCES: 53
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: Februa
                                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                  51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                      17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-3/1-2540
51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guastella, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    February 11, 1997
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99.482
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seq_documentation_block:
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Guaste
                                                       ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08978523 Patent No. 5883229
                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/978,523
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501 GCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCCTGG 550
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: herew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   451 TACGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 euAlaAspTrpI1eHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600
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: DC
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IBM PC compatible
                                                                                                                                                                                                 February 11, 1997
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                                                                                                   1483.0140002
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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-798-897-1
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MOLECULE TYPE: US-08-978-523-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-978-523-2 from: 1 to: 579
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Percent Similarity: 99.482
                                          551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                               184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                               501 GCCATCAGTGACGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                   167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                            151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                        451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                     134 eualaaspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                            351 ACTGGTGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                   301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetalaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 579 ba
TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                   TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 1002.00
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DEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   579 base pairs
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                                                                                                                                                                                                                                                                                                                                              400
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seq\_documentation\_block:

Sequence 1, Application US/08798897 Patent No. 5789201

GENERAL INFORMATION:

APPLICANT:

Guastella, John

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; MOLECULE TYPE: cDNA US-08-798-897-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: February 11, CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                    101 GGGAAGGCCCAGCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 New
CITY: Washington
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/798,897
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                                                              251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCCGTCTTGTGGCATTCTTT 300
                                                                                                                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: bot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME:
                                                                                                                                                                                                                                  51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic aci
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                                                                                  84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                       20005
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Esmond, Robert W.

32,893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 98.446
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-978-523-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08978523 ; Patent No. 5883229
                                                                                             ; MOLECULE TYPE: US-08-978-523-1
                                             alignment_scores:
Ratio: 5.161 percent similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 eualaAspTrpTleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Guastella, JOHN
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
TITLE OF INVENTION: Homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 alThrValGlyAlaPhePheAlaSerLys 193
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION: 202-371-2600
                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,8
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: he CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: Februa
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/978,523
                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                 LENGTH:
                   Quality:
Ratio:
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                                                                                                                                                                                 579 base pairs
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                                    996.00
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                                                                                                                                                                                                                                                                                                 32,893
     percent Identity: 98.446
                                                                                                                                                                                                                                                                                       1483.0140002
                                           Length:
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alignment\_block: US-09-155-327E-7 x US-08-978-523-1

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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-081-448-5
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                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08081448 Patent No. 5646008
                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Thompson, Craig B.

APPLICANT: Boise, Lawrence H.

TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-978-523-1 from: 1 to: 579
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                         551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501 GCCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGCCCTGG 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT 400
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                                                                                                         STREET: 321 No
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 250
                                                    ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 GACGAGTTTGAGACCCGCTTCCGGCGCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 GGGAAGGCCCAGCCGACCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                   COUNTRY:
                                                                                            STATE:
                                                                                                                      ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5646008th Clark Street, Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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alignment_block:
US-09-155-327E-7 x US-08-081-448-5
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Ratio: 3.018
Percent Similarity: 63.393
550 GCATTGTGGCCTTTTTCTCCTTCGGCGGGCACTGTGCGTGGAAAGCGTA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 312-755-4489 INFORMATION FOR SEQ ID NO:
                                                                        500 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC
                                                                                                                                                    400 CGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTC 449
                                                                                                                                                                                                                                                                                                            350 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGCAAG
                                95 rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
                                                                                                                                                                                                                                                                                                                                                                                      300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAAGAACAGGACTGAGGCCCCAG 249
                                                                                                78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                                                         62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 CGGGAGCTGGTTGACTTTCTCTCCTACAAGCTTTCCCAGAAAGGATA 199
                                                                                                                                                                                                                                                     45 laMetargalaalaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                                               41 .....ProLeuHisGlnA 45
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 .....ValCysGlyAlaGlyPro 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 312-744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: NO. 5646008thrup, Thor
REGISTRATION NUMBER: 33 268
REFERENCE/DOCKET NUMBER: ARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
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TELEPHONE: 312-755-4489
To To NO:
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FILING DATE: 199306
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135..836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARCD090
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-470-670A-6
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alignment_scores:
    Quality:
    Ratio:
                                                                                                      US-08-470-670A-6
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                                                                                                                                                                                                                                                            TELEFAX: (514) 4/4-5/1.
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 AsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetValAl 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/470,670A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENTITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Thompson, Craig B. B. APPLICANT: Boise, Lawrence H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION IMPORMATION:
TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                             NAME/KEY:
                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houston
                                                                                                                                                                                                                                                                                                                                                                                                                           Highlander, Steven L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                  : (512) 418-3000
(512) 474-7577
                                                                                                                             CDS
135..836
                                                                                                                                                                                            linear
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  428.50
3.018
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alignment_block:
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                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-481-739-1
PATENT NO. CATALLA PROTEIN:
GENERAL INFORMATION:
GENERAL THEORY JUNE, CARI H. and Thompson, Craig B.
APPLICANT: JUNE, CARI H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
TITLE OF SECHENCES: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600 GACAAGCAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC 649
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                                                                                                                                                                                                                                                                                                          176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                      750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                                                                                                                                                                                                                                                                               162 LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 rgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSerVal 111
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alignment_block:
US-09-155-327E-7 x US-08-481-739-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 3.105
Percent Similarity: 61.333
                                      397 AAGCGCTGAGGGAGGCGACGACTTTGAACTGCGGTACCGGCGGGCA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                  347 CAGCAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGC 396
                                                                                                                                                                                             300 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCC...ACTGGCCA 346
                                                                                                                                                                                                                                                                        250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                                                                                                                                                    200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                               150 CGGGAGCTGGTTGACTTTCTCTCCTACAAGCTTTCCCCAGAAAGGATA 199
61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                             44 lnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThr 60
                                                                                                                                                      35 uGlyProAlaAlaAsp.....ProLeuHisG 44
                                                                                                                                                                                                                                                                                                             27 ...... 27
                                                                                                                                                                                                                                                                                                                                                                                         11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
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LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS; single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,518
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DeConti, Giulio A. (G
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Polon-
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135..836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (617)227-7400
(617)742-4214
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alignment_block:
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; LOCATION: (135)..(836)
; PUBLICATION INFORMATION:
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-167-921-1
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    Patent No. 6172216
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                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTIO: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILLING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    797 CGGCGTGGTTCTGCTGGGCTCACTC 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 ArgLeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 CACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCT 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 GTAGACANGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGC 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 ValAsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetVa 127
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                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                            428.50
3.018
63.393
                                                                                                                                                                                                         Percent Identity: 40.625
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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-277-020-39
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                                    GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: of mRNA Processing
TITLE OF INVENTION: of mRNA Processing
TILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTMARE: PatentIn Ver. 2.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/09277020 Patent No. 6210892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 CGGGAGCTGGTGGACTTTCTCTCTCTACAAGCTTTCCCAGAAAGGATA 199
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TYPE: DNA
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                    ENGTH: 926
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; ORGANISM: Homo sapiens US-09-277-020-39
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US-09-155-327E-7 x US-09-277-020-39
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                                                                                                                                                                                                                                                      145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                            650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
                                                                      800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                         176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                               750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                                                              162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                     700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCCGAGAGCCGAAAG 749
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3.018
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US-09-155-327E-7 x US-09-323-743-1
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; LOCARION: (135)..(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-323-743-1
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LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SED ID NOS: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0368
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                                       78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                    62 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
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                                                                                                                                                                                                                            45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
                                                                                                                                                                                                                                                                                                                    41 .....ProLeuHisGlnA 45
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3.018
63.393
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US-08-461-511A-6
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                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: ARCD:179
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          800 CGTGGTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 yAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       750 GGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCGG 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 LeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuThrG1 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                700 ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       650 TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 GACAAGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetValAl 128
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            SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thompson, Craig B.B.

Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                   LENGTH: 926 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                    NAME/KEY: CDS
LOCATION: 135..836
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND METHODS
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alignment\_scores:

Quality: 428.50

Length:

## us-09-155-327e-7.p2n.rni

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TELEPHONE: 512-320-7200
TELEPAX: 713-789-2679
TELEPAX: 713-789-2679
TELEPAX: 926 DINO: 6:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS: 5:
LENGTH: 926 base pairs
LENGTH: 926 base pairs
LENGTH: nucleic acid
TYPE: nucleic acid
TYPE: 5167ANDEDNESS: 5ingle
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PRIOR APPLICATION UNMBER: 08/081.448

APPLICATION UNMBER: 1993

FILING DATE: 22 JUNE 1993

FILING DATE: 1908

ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,165

REGISTRATION NUMBER: ARCD090

REGISTRATION THEODMATTON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
ADDRESSE: P.O. Box 4433
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US94-07089-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIF: 77210

ZIP: 77210

COMPUTER READABLE FORM:
COMPUTER: Flopy disk

COMPUTER: PC COMPUTER:
COMPUTER: CONCURRENTLY FILED
APPLICATION LOATH:
CONCURRENTLY FILED
APPLICATION CONCURRENTLY FILED
APPLICATION LOATH:
CONCURRENTLY FILED
                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-155-327E-7 x PCT-US94-07089-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               percent similarity:
                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: PCT-US94-07089-6 from: 1 to: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 135..836
                                                                                                                                                                                                                                                                              200 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAGAACAGGACTGAGGCCCCCAG 249
                                                                                                                                                    28 .....AlcysGlyAlaGlyProGlyGl 35
28 .....AcTeGccA 346
300 TCCTGGCACCTGGCAGACAGCCCGCGGTGAATGGAGCC...ACTGGCCA 346
                                                                                                                                                                                                                                                                                                          27 F...... 27
                                                                                                                                                                                                                  250 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 299
                                                                                                                                                                                                                                              27 ...... 27
                            347 CAGCAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGC 396
                                                                                                                    35 uGlyProAlaAlaAsp.....proLeuHisG 44
61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428.50 Length: 24
428.50 Gaps: 3.105
61.333 Percent Identity: 41.333
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APPLICATION NUMBER: US 08/124,256
PRIOR APPLICATION NUMBER: US 08/124,256
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
APPLICATION NUMBER: US 07/840,716
PRIOR APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-198
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-198
NAME: FOITHEY, AGENT INFORMATION:
REGISTRATION NUMBER: 34,600
TELEGOMMUNICATION INFORMATION:
TELLERNICE, DOCKET NUMBER: 3335-070-55
TELLERHONE: (408) 436-2075
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/465,485A
CLASSIFICATION: 514
DDTTO ADDITION TAWAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-465-485A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTON: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                             CLASSIFICATION DATA.
PRIOR APPLICATION DATA.
US 08/124,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/08465485A
Patent No. 5831066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       797 CGCCGTGCTTCTGCTGGGCTCACTC 821
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 rGlyAlaValAlaLeuGlyAlaLeu 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            747 AAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGC 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 ArgLeuArgGlu......GlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697 GGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCAGCCGAGAGCCGA 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647 CACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCT 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 IAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              497 GAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 TTCAGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpG 94
                                                                                                                                                                                                                                                                                                                                                                                      Virginia
Y: U.S.A.
                                          3335-070-55 CONT
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Ignment_scores: Quality: 4: Ratio: 2: Postis-agra-7 x US-0 Ignment_block: -09-155-327E-7 x US-0 Ign seg 1/1 to: US-00 Ign seg 1/1 to	ORMATION EQUENCE LENGTH: TYPE: STRANDE TOPOLOG: LECULE: NAME/KEY LOCATION 65-4850

Thu Jun

6 16:39:21 2002

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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-080-285-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6040181
GENERAL INFORMATION:
                                                alignment_scores:
                                                                                                     US-09-080-285-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 20, Application US/09080285
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616 ATGCGGCCTCTGTTTGATTTCTCCTGGCTGTCTCTGAAGACTCTGCTCAG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   666 TTTGGCCCTG...GTGGGAGCTTGCATCACCCTGGGTGCCTATCTGAGCC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 rGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  713 ACAAG 717
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                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 22-DEC-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
                                                                                                                                                         FEATURE:
                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/840,716 FILING DATE: 21-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/124,256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/080,285
                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                 Quality:
                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                         Fortney, Andrew D
                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: P.C.
1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                 : (408) 436-2070
(408) 436-2075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                         CDS
                                                                                                                          1..717
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22-DEC-1988
                                                                                                                                                                                                          single
   59.574
                  410.50
2.932
                                                                                                                                                                                                                                                                                                                                                                    34,600
   Percent Identity: 37.021
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                                         Length:
                          Gaps:
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alignment_block:
US-09-155-327E-7 x US-09-080-285-20
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                                                                                                                      seq_name: /cgn2_6/ptodata/1/ina/backfiles1.seq:5459251-1
                                                                        seq_documentation_block:
;Patent No. 5459251
; APPLICANT: Tsujimoto, Yoshide;Croce, Carlo A.
; TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 GCCGCATCCCGCGACCCGGTCGCCAGGACCTCGCCGCTGCAGACCCCGGC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 CCCCGCACCGGGCATCTTCTCCTCCCAGCCCGGGCACACGCCCCATCCA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 TGCCCCGGCGCCGCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 GGCGACTTCGCCGAGATGTCCAGCCAGCTGCACCTGACGCCCTTCACCGC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 GACAACCGGGAGATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 GCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGGGTGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 .....proGlyGlu...... 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 GGGCTACGAGTGGGATGCGGGAGATGTGGGGCGCCGCGCGCCCCGGGGGGCCG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 sGlyTyrValCysGlyAlaGly.......32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       528 GATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 GAGAGCGTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTG 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 GluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnGluTr 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 euHisGlnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPheArg 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 ....... GlyproAlaAlaAspPro...... 42
                                                                                                                                                                                                                                                                                                                              175 rGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaS 192
                                                                                                                                                                                                                                                                                                                                                                                 616 ATGCGGCCTCTGTTTGATTTCTCCTGGCTGTCTCTGAAGACTCTGCTCAG 665
                                                                                                                                                                                                                                                                                                                                                                                                                               159 AlaArgArgLeuArgGluGlyAsnTrpAlaSerValArgThrValLeuTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578 GAGGCTGGGATGCCTTTGTGGAACTGTACGGC......CCCAGC 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 lyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGlu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 pMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 snTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAla 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 ArgThrPheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAl 75
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                                                                                                                                                                                                                                                                              666 TITGGCCCTG...GTGGGAGCTTGCATCACCCTGGGTGCCTATCTGAGCC 712
                                                                                                                                                                                  713 ACAAG 717
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SEQUENCES

NUMBER OF SEQUENCES: 4

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alignment_block:
US-09-155-327E-7 x 5459251-1
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Ratio: 2.932
Percent Similarity: 59.574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; SEQ ID NO:1:
1986 GATGACTGAGTACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACG 2035
                                                                                                                               109 GluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnGluTr 125
||||||||||||:::|||||:::|||||||::::::
1936 GAGAGCGTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTG 1985
                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/228,704

FILING DATE: 18 APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 994,941

FILING DATE: 23-DEC-1992

APPLICATION NUMBER: 663,010

FILING DATE: 19-MAR-1991

APPLICATION NUMBER: 883,687

FILING DATE: 09-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                     125 pMetValAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerG 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1486 GACAACCGGGAGATAGTGATGAAGTACATCCATTATAAGCTGTCGCAGAG 1535
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Copyright (c) 1993-2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est1:AA596919
gb_est2:BF204905
gb_est2:BE508939
gb_est2:BE5677345
gb_est1:AW326901
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-Q-/cgn2_1/USPTO_spool/US09155327/runat_06062002_084851_18477/app_query.fasta_1.508
-Q-/cgn2_1/USPTO_spool/US09155327/runat_06062002_084851_18477/app_query.fasta_1.508
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-GAPEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-DELEXT=7.000 -TRANS=human40.cdi
-DELEXT=7.000 -TRANS=human40.cdi
-DELEXT=7.000 -TRANS-human40.cdi
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Database length: -1841457050
Search time (sec): 2329.970000
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gb_est1:AL632408
gb_est2:BM457276
gb_est2:BE293685
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       AKO15644 Mus musculus adult ma

AKO04680 Mus musculus adult ma

AL157542 DKFZp76LD0816_r1 761 (

BI770566 603060362F1 NIH_MGC_12

BI770566 603060362F1 NIH_MGC_13

AKO13244 Mus musculus 10, 11 da

BI910270 603069493F1 NIH_MGC_11

BI910270 603069493F1 NIH_MGC_94

BEC298789 602396527F1 NIH_MGC_94

AW258810 um74202.y1 Sugano mous

BI764428 603950701F1 NIH_MGC_11

BM191403 daj86310.y1 NICHD XGC

AA596919 vo21f08.r1 Barstead mc

BEC2044905 601866718F1 NIH_MGC_17

BE508939 dc14h09.y1 NICHD XGC

AA596912 20104 MARC 2BOV Bos ta

BB65021 BB65021 RIKEN full-1c

AL632408 AL632408 XGC-gastrula

BA457276 AGENCOURT_6406769 NIH_

BE293685 601189941F2 NIH_MGC_15

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BG293530 602042335F1 NIH_MGC_15

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BE250036 600943041F1 NIH_MGC_15

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BG285707 2213 NICHD Zebrafish in

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BG2927101 602943465F1 NIH_MGC_4
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BM193253 TCBAPLE12081 Pediatrid
BM193253 TCBAPLE12081 Pediatrid
AWL59063 za50h02.x1 xenopus ES7
BG470667 602511594F1 NIH_MGC_16
BJ060637 BJ060637 NIBB MOChii
BG180671 602329448F1 NIH_MGC_91
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gb_est2:BF448405
gb_est2:BM193252
gb_est1:BE207063
gb_est2:BF569393
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Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib_RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, K., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
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The RIKEN Genome Exploration Research Group Phase II Team and the
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Submitted (10-JUL-2000) roshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) roshihide Hayashizaki, The Institute of Exploration and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama
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                                                                                                                                     Hayashizaki,Y.
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                                                                                                                     182 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 231
                                                                                                                                                                                        51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                     34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                         17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="bab29912.1"
/db_xref="GI:12854053"
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GAALCARSVKKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVKTVLTGAVALGALYTVGAFFASK"
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/clone_lib="RIKEN_full-length enriched mouse cDNA library"
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/db_xref="taxon:10090"
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Shikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., Sayana, M., Sayana, M.
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Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200009L24:Bcl2-like 2, full insert sequence.
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High-efficiency full-length cDNA cloning
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                                                                       polyA_signal
polyA_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-25 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FANTOM Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11076861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax:81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XhoI. Host: SOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="MGD:MGI:1896837"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                              data source:MGD, source key:MGI:108052, evidence:ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Bc1212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
    /note="putative" 3487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="1200009L24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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AMRAGDEFETRERTFSDLAAQLHYTPGSAQQRFTQVSGCRWGRTYALYCGGALEEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Bc1212"
                                                                                       3466
                                                                                                                     RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 100.000
                                                                                                                        seq_name: gb_est2:BE793530
                                                                                   seq_documentation_block:
LOCUS BE793530
                                                                     DEFINITION
            KEYWORDS
SOURCE
                            VERSION
                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                      117 oLeuvalGlyGlnvalGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                 559 TTTGGTGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                          151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                        709 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCCTGG 758
                                                                                                                                                                                                                                           167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                          TACGGGGACGGGGCCCTGGAGGAGGGCACGGCGTCTGCGGGAGGGGAACTG 708
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                                                                      601590016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307 5',
                                                           mRNA sequence.
 human.
                             BE793530.1 GI:10214832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 98.964
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alignment_block:
US-09-155-327E-7 x BE793530
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ORIGIN
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394 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 443
                                                                                                 344 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCC 393
                                                                                                                                                                                                                        294
                                                                                                                                                                                                                                                                                               244 GGGAGGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 293
                                                                                                                                                                                                                                                                                                                                                                                                194 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 193
                            84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                              67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                          51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                            34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                           17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM800 row: p column: 04
High quality sequence start: 5
High quality sequence stop: 709.
Location/Qualifiers
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DHIOB (phage-resistant)"
/note="organ: lung; Vector: pOTB7; Site_1: xhoI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Stratagene) and Superscript II RT (Life Technologies)."
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/tissue_type="small cell carcinoma"
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BASE COUNT
                                                                                 alignment_scores:
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       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    644 GCCATCAGTGAGGACAGTGCTGACGGGGGGGGGGTGGCACTGGGGGGGCCTGG 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeu. 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     694 GTAACTGTAGGGGCCTTT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 ValThrValGlyAlaPhe 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             594 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGGAGGGGACTG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 eualaaspTrp11eHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@kkfz-heidelberg.de; sequenced by EMBL (Buropean Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                  This clone (DKFZp761D0816) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140: Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 804)
Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No s1 sequence available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Ansorge W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKF2p761D0816_r1 761 (synonym: h
DKF2p761D0816 5', mRNA sequence.
AL157542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                     Ratio:
                                                                                                                                                                          150
       4.964
99.482
                                                                                                                                                         /lab_host="DH10B"
/note="Vector: pSportl; Site_1: NotI; Site_2: SalI"
/ 217 c 294 g 142 t 1 others
                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/clone="DKFZp761D0816"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
                                                      953.00
Percent Identity: 99.482
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alignment_block:
US-09-155-327E-7 x AL157542
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                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est2:B1770566
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                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGCAGCTGGA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584 TACGGGGACGGCC.CTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                            184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 GCCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACT.GGGGCCCTGG 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                         682 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA 583
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 697)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                          603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5'
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                   BI770566.1 GI:15762144
                                                                                                                                                                                                                                                                           mRNA sequence.
                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                       697 bp
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-15\overline{5}-327E-7 \times BI770566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 244
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                                                  395 ATGAACTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 444
                                                                                                                                                                                                                                                                                                                                                    345 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 344
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133 gLeuAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
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                                                                                                                                                                                                                                                                                                                                                                                                    67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                              84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 21 High quality sequence stop: 695.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /incle="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled lung and spleen; RNA source
Site_1: Not1; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
anonymous pool of 24 week female lung, 16 week female
primed and directionally cloned (EcoRV site is destroyed
primed and directionally cloned (EcoRV site is destroyed
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:5209862"
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/db_xref="taxon:9606"
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4.890
97.326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545 GCTGGCTGACTGGATCCACAGCAGTGGGGGGTGGGCGGAGTTCACAGCTC 594
Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Womura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
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                                                                                                                                                                                                                                                                    Nature 409, 685-690 (2001) 5 (bases 1 to 854)
                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                          The RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.
                                                                                                                                                                                                                                                                                                                                                 FANTOM Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibata, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11042159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci, P. and Hayashizaki, Y. High-efficiency full-length cD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKO13244 854 bp mRNA linear HTC 19-JAN-2002 Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone:2810435A13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK013244.1 GI:12850487
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                                                                                                                                                                                                                                                                                                                                                                                                       (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 (11), 1757-1771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                full-length cDNA cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (2000)
                                       Quackenbush, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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Align seg 1/1 to: AK013244 from: 1 to: 854
                                                                                                                                                                                                                                                                                                       US-09-155-327E-7 x AK013244
                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
246 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                              196 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 245
                            17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                      1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues. First strand cDNA was primed with a primer [5' GACAGAGAGAGCCCAGAGACTCTTTTTTTTTTTTTVN 3'], cDNA was primer prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yo
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOST: SOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Gro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax:81-45-503-9216
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5.142
98.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="matpastpdtralvadevgyklrokgyvcgagpgegpaadplho
AMRAAGDEEETRERRTESDLAAOLHVTPGSAQORETOVSDELFOGGPNWGRLVAFEVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB28740.1"
/db_xref="GI:12850488"
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196. .732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Bcl2-like 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Bc1212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="MGD:MGI:1902183"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 95.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 g
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seq_name: gb_est2:BI910270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    496 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                446 ACGAACTTTTCCAAGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 GCTACACGTGACCCCAGGCTCAGCCCAGCTTCACCCAGGTTTCCG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGTAAGAAGTTCTCAATTG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 643)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     643 bp mRNA linear EST 16-OCT-2001 603069493F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5',
                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11548 row: j column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: Location/Qualifiers
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV of (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note:
                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:5218294"
/clone_lib="NIH_MGC_118"
                                                                                                                                                                                                /tissue_type="leukocyte"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                    643.
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                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                         VERSION
                          COMMENT
                                                                                                                          REFERENCE
                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                   ORGANISM
                                                                           TITLE
                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGCATGGAAC 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGlu.MetGluP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 uTyrGly.....AspGlyAlaLeuGluGluAlaArgArgLeuArgGlu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 LeuAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 CACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGCTGACTGGATCCACAGCAGTGGGGGGCTGG...GAGCTGGAAGCTAT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est2:BF785386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                 5', mRNA sequence.
BF785386
                                                                                                                                                                                                                                                                                                                                             602111728F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
                                                                                                                                                                                                                                                                       BF785386.1 GI:12090422
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                            Contact: Robert Strausberg, Ph.D.
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 815)
                                                 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                  NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                          house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this is a NIH_MGC Library."
a 184 c 216 g 114 t
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4.831
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                                                                                                                                                                                                                                                                                                                                                                               815 bp
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                                                                                                                                                                                                                                                                                                                                                                                 mRNA
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DEFINITION

SOURCE VERSION

ORGANISM

KEYWORDS

EST

REFERENCE

TITLE

JOURNAL AUTHORS

FEATURES

linear

EST 12-JAN-2001

source

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: BF785386 from: 1 to: 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-155-327E-7 x BF785386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                       141 erGlyGlyTrpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGlu 157
                  397
                                                                                                               347
                                                                                                                      124 uTrpMetValAlaTyrLeuGluThrArgLeuAlaAspTrpTleHisSerS 141
                                                                                                                                                                                          298 GCTGAGAGTGTCAACAAAGAAATGGAGCCTTG.GTGGGACAAGTGCAGGA 346
                                                                                                                                                                                                                                        108 AlaGluSerValAsnLysGluMetGluProLeuValGlyGlnValGlnG1 124
                                                                                                                                                                                                                                                                                            251 CTAACTGGGGCCGTCTTGTGGCATTCTTGTCTTGGGGC...TGCCTGTGT 297
                                                                                                                                                                                                                                                                                                                                                                                           201 AGCCCAGCAACGCTTCACCCAGGTTTCCGACGAACTTTTCCAAGGGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 CGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTT.GAGACCCGTTTC 150
                                                                                                                                                                                                                                                                                                                                        91 roAsnTrpGlyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCys 107
                                                                                                                                                                                                                                                                                                                                                                                                                     74 rAlaGlnGlnArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 roLeuHisGlnAlaMetArgAlaAlaGlyAspGluPheGluThrArgPhe 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 GAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGACC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 nLysGlyTyrValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 ProAspThrArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGl 24
                                                                                          TTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCA 396
GTGGGGGCTGGGGGTTCACAGCTCTATACGGGGACGGGCCCCTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence start: 3 High quality sequence stop: 650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: LLAM9853 row: h column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library. | "
a 212 c 296 g 141 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.114
96.774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:4239798"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 91.398
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ORIGIN

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alignment_block:
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                                                                                                                                                                    Align seg 1/1 to: BG298789 from: 1 to: 792
                                                                                                                                                                                                                     US-09-155-327E-7 x BG298789
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                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est2:BG298789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                       99 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 148
                                                                                                              1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 uThrGlyAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      544 TAGCACGT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 laSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 GACGGGGCCCTGGCACT.GGGGCCCTGGTAACTGTAGGGGCCCTTTTTGC 543
                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://image.llnl.gov
Plate: LLAM10394 row: e column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BG298789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NLH_PNU____/
/clone_lib="retina"
/tissue_type="retina"
/tissue_type="retina"
/tissue_type="retina"
/tissue_type="retina"
/tissue_type="retina"
/tissue_type="retina"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
246 g 171 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 a
                                                                                                                                                                                                                                                                                         99.315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:4511215"
/clone_lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                     733.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                  5.055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 97.945
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149 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 198

lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50

3 4

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seq_name: gb_est1:AW258810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 GCTACACGTGACCCCAGGCTCAGCCCAGCTTCACCCCAGGTTTCCG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGC.GCTCA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 TGGCTGACTGGATCCACAGCAGTGGGGGCTGGTAAGAA 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 TTTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTC 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyTLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGlu 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW258810 540 bp mRNA linear EST 23-E um74a02.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2300906 5' similar to SW:BCLM_MOUSE P70345 APOPTOSIS REGULATOR BCL-W. [2] SW:BCLM_MOUSE;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 540)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
Underwood, K., Steptoe, M., Theising, B., Allen, M., Schurk, R., Ritter
, B., Swaller, T., Gibbons, M., Pape, D., Harryey, N., Schurk, R., Ritter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW258810.1 GI:6631791
                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse
                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                  MGI:1009678
                                                                                                                                                                                                                                                                       primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                314 286 1800
314 286 1810
                                                                                                                                                                                                                                            quality sequence stop: 465.
                                                                     /clone_lib="Sugano mouse kidney mkia"
                  /sex="female"
/dev_stage="adult"
                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:2300906"
                                                                                                                                                 /strain="C57BL
                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                            OCA L
/lab_host="DH10B"
                                                                                                                                                                                                                            on/Qualifiers
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SOURCE

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alignment_block:
US-09-155-327E-7 x AW258810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AW258810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                     seq_name: gb_est2:BI764428
                                                                                                                               seq_documentation_block:
KEYWORDS
                     VERSION
                                        ACCESSION
                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 GGGAAGGCCCAGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 261
                                                                                                                                                                                                                                                                                                                                                    117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                               134 euAlaAspTrpIleHisSerSerGly 142
                                                                                                                                                                                                                                                                                                           462 TTTGGTGGGACAAGTGCATGATTGGATGGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSorAspLeuAlaAlaGl 67
                                                                                                                                                                                                                       512 TGGCTGACTGGATCACAGCAGTGGGG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTACACGTGACCCCAGGCTCAGCCCAGCCACGCTTCACCCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                 603050701F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5',
EST
                     BI764428.1 GI:15756006
                                                                mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: kidney; Vector: pME188-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA (CACTGTGTG); site_1: DraIII (CACCATGTGG); 1st strand cDNA was primed with an oligo(dT) primer was primed with an oligo(dT) primer was primed with an oligo(dT) primer for the category of the pME18s-FL3 and cloned into distinct DraIII sites of the pME18s-FL3 and cloned into distinct DraIII sites of the pME18s-FL3 and cloned into distinct DraIII sites of the pME18s-FL3 be used to isolate the cDNA insert. Size selection was be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library performed to exclude fragments <1.5kb. Library of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGAACCAA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
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5.107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 95.070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 g
                                                                                                                   758 bp
                                                                                                                          mRNA
                                                                                                                               linear
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                                                                                                                            EST 25-SEP-2001
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alignment_block:
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: BI764428 from: 1 to: 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-155-327E-7 x BI764428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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389 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 438
                                                                                               339 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 388
                                                                                                                                                                                                                 289
                                                                                                                                                                                                                                                                                            239 GGGAGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 288
                                                                                                                                                                                                                                                                                                                                                                                            189 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                           67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                            51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                      34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                         17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                  GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://image.llnl.gov
Plate: LLAM11477 row: a column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="organ: pooled colon, kidney, stomach; Vector:
pcMV-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583.00
5.205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:5190792"
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 to 758)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                           US-09-155-327E-7 x BM191403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
210 CAGCTATGCGTGCTGCAGGGGATGAATTTGAGGAGCGATTCAGACAAGCA 259
                                                                                            169 TGTT.....CCAGAGCCTGCAGGACCAGCATCCTGTGCTTTGCATT 209
                                                                                                                                                                                        119 CGGGCTTTGGTGGAGGATTTTGTGCGGTACAAGTTATGCCAACGTAGTCT 168
                           27 rValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspProLeuHisG 44
                                                                                                                                                                                                                                  11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40Rp from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM191403 601 bp mRNA linear EST 11-DEC-20 daj86a10.yl NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:5129754 5' similar to SW:AR1_XENLA Q91827 APOPTOSIS REGULATOR R1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM191403.1 GI:17527366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 601)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC 1 125 c 189 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                              571.50
4.112
84.756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:5129754"
/clone_lib="NICHD XGC Li1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                         from: 1 to: 601
                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 66.463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
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seq_name: gb_est1:AA596919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 ACGATTTGCTGAAGTAGCAGGTAGCCTGTTCCAAGGAGGGGTGAATTGGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 TTCAGTGAGATCTCCACACAGATCCACGTGACCCCGGCACAGCATATGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 lAlaTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 GGCGTATAGTTGCATTTTTTGTTTTTTGGTGCCGCACTGTGTGCTGAGAGT 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 GACATATCTGGAGACAAACCTGAGAGGCTGGATTCAGAGCAATGGAGGCT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 lyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSer 110
                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpAlaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA596919

AA596919

TO 21f08.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone mage: 1050567 5' similar to TR:E123735 E123735 R1 MRNA. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA596919.1 GI:2412354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                             seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 334.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
                                                                                                                                                                                                                                                                                   MGI:582143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 362)
                                                                                                                                                                                                                                                                                                                                                                        314 286 1800
314 286 1810
                                                                                                                                                                                                                                                                                                                                               mouseest@watson.wustl.edu
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:1050567"
                                                                   /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
                                                                                                                                                      /strain="C3H
                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
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ORGANISM
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SOURCE

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est2:BF204905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 GCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGTGCTGCTGGAGACGAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 GlyAlaAlaLeuCysAlaGluSerValAsnLys 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 GGGGCTGCCCTGTGTGCTGAGAGTGTCACAAAG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 TTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTTGTCTTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 CTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 yTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProGlyGluG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 lyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGlyAspGlu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 eupheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePheValPhe 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 sValThrProGlySerAlaGlnGlnArgPheThrGlnValSerAspGluL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 ThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPheValG1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                            601866718F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106836 5',
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 601)
                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                 NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                        BF204905.1 GI:11098491
                                   Tissue Procurement: ATCC
                                                       Email: cgapbs-r@mail.nih.gov
                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                               Unpublished (1999)
cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characteristic muscle proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rapidly, forming contractile myotubes and producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library constructed by Bob Barstead. The CZCLZ cell line Library constructed by Bob Barstead. The CZCLZ cell line (available from ATCC, catalog # CRL-1772) differentiates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (available from ATCC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   570.00
5.135
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                                                                                                                                                                                                                                                                                                                                                         601 bp
                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                             linear
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seq_name: gb_est2:BE508939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                       134 uAlaAsp.TrpIleHisSerSerGlyGly 143
                                                                                                                                      515 CTGGTGGGACAAGTGCAGGAGTGGATGGTGGCTACTGTGAGACGCGGTCT 564
                                                                                                                                                                                      118 LeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgLe 134
                                                                                                                                                                                                                                            465 TCTTGGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCA 514
                                                                                                                                                                                                                                                                        101 alPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPro 117
                                                                                                                                                                                                                                                                                                                                                      415 GAACTGTTTGCAAGGGGGCCCCAACTGGGGTTCGCTTGTAGCCTTCTTGG 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                              365 TCATGTGATCCCAGGCTCAGCCCAACAACGACTTCACCCAGGTCTCCGAT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 GTTCGAGACCCGCTTCCGGCGTCACCTTCTCTGATCTGGCGGCTCAGCTG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 GGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGAGATGA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 GTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 CCAGCCTCGGCCCCAGACCACAACCGGGCTCTGGTGGCAGACATTTGTAG
                                                                                                                                                                                                                                                                                                                                                                                     85 GluLeuPhe.GlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePheV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 .HisValThrProGlySerAlaGlnGlnArg.PheThrGlnValSerAsp 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 uPheGluThrArgPheArgArg.ThrPheSerAspLeuAlaAlaGlnLeu 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 GlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGlyAspGl 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 lyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProGlyGlu 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ProAlaSerAlaProAsp...ThrArgAlaLeuValAlaAsp.PheValG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                            GGCTGATCTGGATCCAAAGAGAGTGGGGT 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM987 row: d column: 05
High quality sequence stop: 561.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; vector: pOFBF; Site_1: EcoRT;
Site_2: XhoI: cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 568.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4106836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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alignment_block:
US-09-155-327E-7 x BE508939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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312 ACGATTTGCTGAAGTAGCAGGTAGCCTGTTCCAAGGAGGGGTGAATTNGG 361
                                                                                                                                                               262 TTCAGTGAGATCTCCACACAGATCCACGTGACCCCCGGCACAGCATATGC 311
                                                                                                                                                                                                                                            171 TGTT......CCAGAGCCTGCAGGACCAGCATCCTGTGCTTTGCATT 211
                                                                                                                                                                                                                                                                                                                               121 CGGGCTTTGGTGGAGGATTTTGTGCGGTACAAGTTATGCCAACGTAGTCT 170
                        77 nArgPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpG 94
                                                                                                                        61 PheSerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnG1 77
                                                                                                                                                                                                                                                                                      27 rValCysGlyAlaGlyProGlyGluGlyProAlaAlaAspProLeuHisG 44
                                                                                                                                                                                                                                                                                                                                                                       11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Seq primer: -40Rp from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE508939 612 bp mRNA linear EST 07-AUG-2000 dC14h09.y1 NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:3397121 5' similar to SW:AR1_XENLA 091827 APOPTOSIS REGULATOR R1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE508939.1 GI:9728714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 612)
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3.908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NICHD XGC Li1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:3397121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 62.651
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161	144	127	111	94
562	512	462	412	362
161 ArgieuArgGluGlyAsnTrpAlaSerValArgThrVaiLeuThrGly 176	rpalaGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArg     :::                TGAATGGATTTCTAACTCTATATGGGGATGGTGCCATAGAAGAAGCCAGG	1AlaTyrLeugluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyT  :::              	ValasnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetVa             :::      ::: 	lyArgLeuValAlaPhePheValPheGlyAlaAlaLeuCysAlaGluSer       :::
	160	144	127	110
	561	51]	461	411

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OM of: US-09-155-327E-7 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                 About: Results were produced by the GenCore software, version 4.5.
                                                                                                                                                                                                                                                                                                                                                                                                            Date: Jun 6, 2002 2:37 PM
                                                                                                                                                                                                                                                                    Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
                                                                                                                                                                                                                                                                                            Search information block: Query: US-09-155-327E-7
                                                                                                                                                                                                                                                                                      Query length: 193
                                                                                                                                                                                                                                                                Search time (sec): 288.150000
                                                                                                                                                                                                                                                                                                           Copyright (c) 1993-2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                          out_format : pfs
                                                                                                           4 1.5e-36
1 3.3e-36
2.1e-35
                                                                                                                             1.5e-36
1.5e-36
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1.5e-36
1.5e-36
                                                                                                                                                                          3.6e-94
3.6e-94
1.5e-72
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1.7e-97
                                    2.0e-33
                                                                                                                                                                                                                             3.9e-98
                                                         1.1e-33
                         2.3e-33
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                                                                                                                                                                                                      6.5e-98
                                                                                                                                                                                                           6.5e-98
                                                                                                                                                                                                                  6.5e-98
                                                               1.1e-33
                                                                                                                                                                     3.0e-72
       2.4e-34
4.1e-34
8.0e-34
                                                                                                                                                        6.3e-37
                                                    1.1e-33
                                                                               9.9e-35
                                                                                            9.0e-35
                                                                                                 9.0e-35
                                                                                                       2.1e-35
                                          1.4e-33
                                                                    2.2e-34
                                                                          .3e-34
                                                                                                                                                               61158
                                                                                                                                    9297
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alignment\_scores

Quality: 1007.00 Katto:

alignment\_block: US-09-155-327E-7 x AAX25132 Align seg 1/1 to: AAX25132

1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17

from: 1

to: 581

Percent Similarity:

100.000 5.218

Percent Identity: 100.000

Length:

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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:AAQ81696+
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV17638+
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:ABA/3433-
seq_documentation_block:
ID AAX25132 standard; DNA; 581 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:AAX25132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             χX
                                                 The present sequence is the human bcl-w gene encoding Bcl-w protein compared to the Bcl-2 family which is compared to the Bcl-2 family which is compared to the Bcl-2 family which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an action in model for the identification of molecules and genetic sequences useful for inducing or reducing fertility, or animals. Methods are provided for the treatment of infertility, or animals. Methods are provided for the treatment of infertility, or model carries a mutation is at least one allele of the human or model carries a mutation is at least one allele of the human or model carries a mutation is at least one allele of the animals infertile, but possess no other major abnormalities as determined to by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility; animal model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bcl-w gene
                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 32; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY05530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams J, Cory S, Gibson L, Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            protein associated with Bcl-w
Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other:
                                        animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97AU-0009228.
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV28334
                                                                                                                                                                                                                                                                                                                                                                                                             documentation_block:
11-FEB-1997;
                                     04-AUG-1998
                                                                       US5789201-A.
                                                                                                                                                                                                                                              ss; bcl-y; bcl-2; cell death pathway; apoptotic;
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                     Human bcl-y gene.
                                                                                                                                                                                                                                                                                                                       02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                             AAV28334;
                                                                                                                                                                                                                                                                                                                                                                                           AAV28334 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GGGAGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCCTTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
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                                                                                                                                                             Location/Qualifiers 1..579
                                                                                                                        /product= bcl-y
                                                                                                                                          /*tag=
                                                                                                          /note=
                                                                                                   "No stop codon given"
                                                                                                                                          a
                                                                                                                                                                                                                                              apoptosis; human
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alignment_block:
US-09-155-327E-7 x AAV28334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAV28334 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu
                                                             351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                         301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                           101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr
                                                                                                                                                                                                                    251 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
                                                                                                                                                                                                                                                                                                201 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                    151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.
                                                                                                                                                                                                                                         84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                     67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
                                                                                                                                                                                                                                                                                                                                                                                              51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Column 15/16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding B-cell lymphoma y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-446079/38
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11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COCE-) COCENSYS INC.
                                                                                 OLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                            GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGAGGGCCCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1002.00
Ratio: 5.219
milarity: 99.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0012201
97US-0798897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 99.482
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                        150
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX15946
The present sequence encodes human bcl-y protein (Hbcl-y). The CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and CC proteins may be used to treat conditions associated with a disruption of CC proteins may be used to treat conditions associated with a disruption of CC used in therapies to treat subjects suffering from: strokes, head trauma, CC used in therapies to treat subjects suffering from: strokes, head trauma, CC especially multiple sclerosis, myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC cell death, aging, spinal cord injuries and amyotrophic lateral as a CC sclerosis- conditions where cells under go premature cell death as a CC cresult of triggers which may or may not be apparent. They may also be CC used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, and amyotrophic lateral conditions associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGCCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 TACGGGGACGGGCCTTGGAGGAGGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's bisease; neural; muscular degenerative disease; head trauma; Alzheimer's bisease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX15946 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding the human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5883229-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                     Disclosure; Columns 15-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                             Novel bcl-y homologues of the rat and human bcl-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                           modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0012201.
97US-0798897.
97US-0978523.
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAX15946 from: 1
seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/Na1999.DAT:AAX25133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                          351
                                                                                                                                                                                                                                                                                                                                                                                           117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                                                                                                                        451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                            151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                       401
                                                                                                                                                                                                                                                                                                                                134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGCCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetalaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                           551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGAGGGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGGAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                       TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                                                          euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                     ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                          GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGGCCCTGG
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5.219
99.482
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seq\_documentation\_block:

AAX25133 standard; DNA; 581

05-JUL-1999 (first entry)

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alignment_block:
US-09-155-327E-7 x AAX25133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see AAY05531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The canimal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male compared to a mimals. Methods are provided for the treatment of infertility, or compared to the treatment of the following or compared to the treatment of the following compared to the following compared 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                                                                                                          101 GGGAAGGCCCAGCCGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA
                               51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                      34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                    51 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                                                                                                  17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                           1 ATGGCGACCCCAGCCTCAACCCCCAGACACGCGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                            1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 34; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F-PSDB; AAY05531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1997;
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GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         animal model; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ing, enhancing or convergentiality.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 1000.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97AU-0009228.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 98.964
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                        Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                           P-PSDB; AAW36047
                                                                                                                                                                                        WPI; 1997-489635/45.
                                                                                                                                                                                                                                                               Adams JM,
                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-1996;
                                                                                                                                                                                                                                                                                                                    (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09735971-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
diagnosis; degenerative disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bcl-w DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT96577 standard; DNA; 583 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 GCCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                    Cory S,
                                                                                                                                                                                                                                                                                                                                                                                       96AU-0008965
                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-AU00199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                             Gibson LM,
                                                                                                                                                                                                                                      Holmgreen SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350
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184 alThrValGlyAlaPhePheAlaSerLys 193
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8 x 222222222222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAT96577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-155-327E-7 x AAT96577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 48; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                 117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                301 CTCTTTGGGGCTGCACTGTGTGCTGAAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                                        101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                    251 ACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGCCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                     euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                       pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                               TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                       TGGTCGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                                                                             ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1000.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 98.964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250
                  550
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/Na1999.DAT:AAX25134
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                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                    alignment_block:
                                                                                                                                                                                Percent Similarity: 100.000
Align seg 1/1 to: AAX25134
                                                                            US-09-155-327E-7 \times AAX25134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX25134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX25134 standard; DNA; 583 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bcl-w gene derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bel-w gene a mutation is at least one allele of the human or murine bel-w gene a mutation is at least one allele of the human or murine bel-w gene a mutation is at least one allele of the human or murine bel-w gene a mutation is at least one allele of the human or murine bel-w gene a mutation may be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including they can be used to screen for therapeutic molecules including the fertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9913710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             animal model;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is described as a derivative of the human bcl-w gene (see AAX05132) and encodes Bcl-w protein (see AAY05532), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the described on the second seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 36; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams J, Cory S, Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p-PSDB; AAY05532.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                     Quality: 1000.00
                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97AU-0009228.
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                                                                                                                                                                                                                                         5.181
                from: 1
                                                                                                                                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koentgen F, Print C;
                    to: 583
                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                     Gaps:
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:AAV28333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                  AAV28333 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          501 GCCATCAGTGAGGACAGTGCTGACGGGGCCCGTGGCACTGGGGGGCCCCTGG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 CTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 ACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GGGAGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaG1 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTCGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                   (first entry)
 96US-0012201
97US-0798897
                                                 97US-0798897
                                                                                                                                                                    /product= bcl-y
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                  /*tag= a
                                                                                                                                                                                                                                                                       cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                                               "No stop codon given"
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 100.000
151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                          401 TGGCTGACTGGATCCACAGCAGTGGGGGGGTTGGGCGGAGTTCACAGCTCTA 450
                                                                134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                           351 ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT
                                                                                                                                                               117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                           301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                 101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                             251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                                                                                                                                                                                                                                                                             201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GGGAAGGCCCAGCAGCCGACCGGCTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                                                                                   84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                  67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity, bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression in vivo. Also, antisense const where prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Column 13/14; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding B-cell lymphoma y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-446079/38.
P-PSDB; AAW61391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     996.00
5.161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Also, antisense constructs can be used in disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 98.446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                             350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAX15945
CC especially multiple sclerosis, mycardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral conditions which way to develop cell lines which means which remains cell death aging, spinal cord injuries and amyotrophic lateral cord in this way to develop cell lines which may or may not be apparent. They may also be creatly and this way to develop cell lines which may or may not be apparent. They may also be creatly and this way to develop cell lines which remain viable in culture for cell meathed period. In contrast, if they act as cell death stimulators, an extended period. In contrast, if they are as cell death with conditions and this way to develop cell lines which remain viable in culture for cell my cancer) and Hbcl-y may be used to treat conditions associated with conged cell life span such as cancer (especially kaposi's sarcoma and conditions cell life span such as cancer (especially kaposi's sarcoma and conditions cell life span such as cancer (especially kaposi's sarcoma and conditions cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA encoding the rat bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX15945 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5883229-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parasite; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guastella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Columns 13-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW97391.
                                                                                                                                                                                                                                                                                                              The present sequence encodes rat bol-y protein (Rbcl-y). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0012201.
97US-0798897.
97US-0978523.
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XEXEXX

22-APR-1998 (first entry)

AAT96578;

Mouse bcl-w DNA

AAT96578 standard; DNA; 581 BP

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 996.00
Ratio: 5.161
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAX15945 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-155-327E-7 x AAX15945
                                     seq_name: /SIDS1/gcgdata/geneseg/geneseqn-emb1/NA1997.DAT:AAT96578
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 579 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GGGAAGGCCCAGCAGCCGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GACGAGTTTGAGACCCGCTTCCGGCGCACCTTCTCTGACCTGGCCGCTCA
                                                                                                                                                                                                                                                                                                                401
                                                                                                                                                                                                                                                                                                                                                                                                             117 oLeuvalGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 ACGAACTTTTCCAAGGGGGCCCCAACTGGGGGCCGTCTTGTGGCATTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 TGTAGGCTATAAGCTGAGACAGAAGGGTTATGTCTGTGGAGCTGGCCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                             167 palaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                      451
                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84
                                                                                                  184 alThrvalGlyAlaPhePheAlaSerLys 193
                                                                                                                                                        501 GGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh
                                                                                  551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                    TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
                                                                                                                                                                                                                                                                                                              TGGCTGACTGGATCCACAGCAGTGGGGGGGCTGGGCGGAGTTCACAGCTCTA
                                                                                                                                                                                                                                                                                                                                  ATTGGTGGGACAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCT
                                                                                                                                                                                                                                                                       TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 98.446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                              450
                                                                                                                                                                                                                                                                                                                                                                                                          400
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alignment_block:
                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                               Align seg 1/1 to: AAT96578 from: 1 to: 581
                                                                                                                                                                                                                                                                                 US-09-155-327E-7 x AAT96578
                                                                                                                                                                                                                                                                                                                             Percent Similarity:
101 GGGAAGGCCCAGCCGACCCGCTGCACCAAGCCATGCGGGCTGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in stroke, alzheiner's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell inas cultured in vivo. e.g. to develop new lines, to facilitate during genetic modification. It can be used to modify cell isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w modulators, diagnosis, antibody production or screening of potential
                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;
                                                                                                                       51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 50-51; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degenerative diseases
                                                                                                                                                                                  1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                  1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW36048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-489635/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09735971-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; degenerative disease; ss.
                                                                                                                                        eValG1yTyrLysLeuArgG1nLysG1yTyrVa1CysG1yA1aG1yProG
||||||||||
                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis; bc1-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96AU-0008965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-AU00199.
                                                                                                                                                                                                                                                                                                                           965.00
5.079
98.446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= bcl-w
/note= "q"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibson LM,
                                                                                                                                                                                                                                                                                                                         Percent Identity: 94.819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holmgreen SP;
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CCXXX PRODUCT CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _documentation_block:
AAX25135 standard; DNA; 581 BP.
                                                Disclosure; Page 38; 52pp; English.
                                                                                                                      protein associated with Bcl-w
                                                                                                                                           An animal model exhibiting reduced levels
                                                                                                                                                                                                                       P-PSDB; AAY05533.
                                                                                                                                                                                                                                                                                                                                                                             (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                       WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09913710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animal model;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse bcl-w gene derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             501 GCCATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 eualaaspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 TTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ValPheGiyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCTGACTGGATCCACAGCAGTGGCCGGCTGGGCGGACTTCACAGCTCTA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACGGGGACGGGCCCTGGAGGACGCACGGCGTCTGCGGGAGGGCAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                                                                                                                                                                                                                                                     Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         97AU-0009228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-AU00764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..507
                                                                                                                                                                                                                                                                                                                  Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ש
                                                                                                                                                                                                                                                                                                              Koentgen F, Print C;
                                                                                                                                of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400
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The present sequence is described as a derivative of the mouse

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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAX25135 from: 1 to: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-155-327E-7 x AAX25135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bcl-w gene (see AAX25133) and encodes Bcl-w protein (see AAX05533), pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for identification of molecules and genetic sequences useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identification or mulecuary .... identification or reducing fertility of male animals. Methods are inducing or reducing fertility, or for reducing provided for the treatment of infertility, or for reducing provided for the treatment of infertility, or for reducing a provided for the treatment of infertility, or for reducing the provided for the treatment of infertility, or for reducing the provided for the treatment of infertility, or for reducing the provided for the treatment of infertility of male animals. Methods are inducing or reducing the provided for the treatment of infertility of male animals. Methods are inducing or reducing fertility of male animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
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                                                                                                                                                                                                                                                                                                                                                                                                         351 TTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
GGCATGAGTGAGCACAGTGGTGACGGGGGCCCGTGGCACTGGGGGGCCCCTGG
                                pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                              TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                         euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                      TACGGGGACGGCCCTGGAGGACGCACGGCGTCTGCGGGGAGGGCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.079
98.446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV41925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID      AAV41925 standard; cDNA; 1098 BP.
                                                                                                                                                   alignment_scores:
                                                                        alignment_block:
                              Align seg 1/1 to: AAV41925
                                                           US-09-155-327E-7 x AAV41925
                                                                                                        Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-1998 (first entry)
                                                                                                                                                                                                                      This is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9831800-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunological disorder; autoimmune disease; anti-infectious agent;
                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feng P,
                                                                                                                                                                                            Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                              or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-414099/35.
P-PSDB; AAW59884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AUCK-) AUCKLAND UNISERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gentz RL, Krissansen GW,
                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0034205.
97US-0034204.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US00960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Bcl-like (HAICH29) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1..1098
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                                                                                                                                        766.00
                                                                                                                         5.319
                                   from: 1 to: 1098
                                                                                                           Percent Identity: 100.000
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                                                                                                                                         Length:
                                                                                                                           Gaps:
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV59630
            02-OCT-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

07-MAR-1997

11-APR-1997
                                                                                                                                                                                                                                             Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; inmune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                               06-MAR-1998;
                                                                                                                                                                      11-SEP-1998
                                                                                                                                                                                              W09839448-A2
                                                                                                                                                                                                                                                                                                                                                                         19-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                 Human secreted protein gene 120 clone HGBGZ64.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAV59630 standard; DNA; 1864 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCTGACTGGATCCACAGCAGTGGGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eValG1yTyrLysLeuArgG1nLysG1yTyrValCysG1yA1aG1yProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolism; regulation; malabsorption; gastritis; neoplasm
          97US-0038621.
97US-0040161.
97US-0040162.
97US-0040163.
97US-0040333.
97US-0040334.
97US-0040336.
97US-0040331.
                                                                                                                        97us-0061060
                                                                                                                                             98WO-US04493
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     22-AUG-1997
                                                                                                                                                                                                         22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                            08-JUL-1997;
16-JUL-1997;
18-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                           23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
06-JUN-1997;
06-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
23-MAY-1997;
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11-APR-1997;
11-APR-1997;
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11-APR-1997
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97US-0056862

97US-0056874

97US-0056874

97US-0056875

97US-0056876

97US-0056876

97US-0056876

97US-0056889

97US-0056880

97US-0056888

97US-0056888
                                                                                                                                                                                          97US-0043670

97US-0043671

97US-0043671

97US-0047501

97US-0047501

97US-0047581

97US-0047582

97US-0047583

97US-0047583

97US-0047584

97US-0047587

97US-0047587

97US-0047587

97US-0047589

97US-0047593

97US-0047594

97US-0047591

97US-0047591

97US-0047513

97US-0047611

97US-0047613

97US-0047633

97US-0046631

97US-0056631

97US-0056631
                                                                                                                                                         97US-0056662.
97US-0056664.
97US-0056845.
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97US-0043313
97US-0043568
97US-0043569
97US-0043578
97US-0043578
97US-0043580
97US-0043580
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101

201

67

84

151

51

101

34 51 17

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a nucleic acid molecule designated Gene 120 from the human cDNA clone HGBCZ64 (deposited as clone ATCC 97902 and ATCC 209048) which encodes a secreted human protein. The gene can be communoglobulin Fc portion (e.g. AAV59502) for increasing the stability of immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 186 novel genes and their fragments (nucleic cacid sequences: AAV5951-V59812; amino acid sequences AAW74731-W75026)

Which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new Collypucleotides. Specific uses are described for each of the 186 the new polynucleotides. Specific uses are described for each of the 186 polypucleotides, based on which tissues they are most highly expressed in
                                                                                                                                                                                       Align seg 1/1 to: AAV59630
                                                                                                                                                                                                                       US-09-155-327E-7 x AAV59630
                                                                                                                                                                                                                                                                   Percent Similarity: 100.000
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22-AUG-1997;
22-AUG-1997;
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22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1997;
22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feng P, Ferrie AM, Fischer CL, Flor
Kyaw H, Lafleur DW, Li Y, Moore PA,
Ruben SM, Shi Y, Soppet DR, Young P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 353-354; 721pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bednarik DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                               Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other;
   111
11 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 60
                                                                                                                                            1 MetalaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-506364/43.
                                                               TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                              AAV59511 for described uses).
                                                                                                                                                                                                                                                                                                    Quality:
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                                                                                                                                                                                                                                                                                       Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0056886.
97US-0056887.
97US-0056888.
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                                                                                                                                                                                                                                                                                     766.00
5.319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0056908.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0056911.
                                                                                                                                                                                            from: 1 to: 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carter KC,
                                                                                                                                                                                                                                                                        Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KC, Duan R, Ebner R, Florence KA, Greene J. e PA, Ni J, Olsen HS,
                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Greene JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zeng Z;
                                                                      110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA;
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:ABL32228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirhidammatory; cancer; eye disease; arteriosolerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ValpheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL32228 standard; DNA; 6049 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiarteriosclerotic; antianaemic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                             30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                             WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                Claim 1; SEQ ID NO 201;
                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                WPI; 2002-130909/17.
                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                      02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCTGACTGGATCCACAGCAGTGGGGGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune system disease; cytosine methylation;
                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                 32pp + Sequence Listing;
                                                                                                                                                                                             Berlin
                                                                                                                                                                                                <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nootropic;
                                                                                      German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

macular degeneration, arteriosclerosis,

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seq_documentation_block:
ID AAS00247 standard; DNA; 1236 BP
                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAS00247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-155-327E-7 x ABL32228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: ABL32228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5351 ATTGGTGGGATAAGTGTAGGAGTGGATGGTGGTTTATTTGGAGACGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5151 GATGAGTTCGAGATTCGTTTTCGGCGTATTTTTTTTTTGATTTGGCGGTTTA 5200
Chimeric - Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5101 GGGAGGGTTTAGTAGTTGATTCGTTGTATTAAGTTATGCGGGTAGTTGGA 5150
                Chimeric - Corynebacterium diptheriae
                                       Chimeric - Homo sapiens
                                                                                           Human; Bcl-Xl-DTR; apoptosis; cancer; spinal muscular atrophy; ds; diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                      Huntington's disease
                                                                                                                                                                                                           Bcl-xl-DTR apoptosis-modifying fusion protein, DNA sequence.
                                                                                                                                                                                                                                                                   31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 euAlaAspTrpIleHisSerSerGlyGlyTrp 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5001 ATGGCGATTTTAGTTTCGGTTTTAGATATACGGGTTTTGGTGGTAGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTTTTGGGGTTGTATTGTGTGTTGAGAGTGTTAATAAGGAGATGGAATT 5350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
||||||:::||| |||||| ||||||||||:::|||:::|||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGTTGATTGGATTTATAGTAGTGGGGGTTGG 5432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAATTTTTTAAGGGGGTTTTAATTGGGGTCGTTTTGTAGTTTTTTT 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTAGGTTATAAGTTGAGGTAGAAGGGTTATGTTTGTGGAGTTGGTTTCG 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444.00
3.795
81.250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
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The sequence represents the coding sequence of Bcl-Xl-DTR apoptosis-CC modifying fusion protein comprising human Bcl-Xl sequence fused via a CC short linker to diphtheria toxin receptor binding domain (DTR). The CC functional apoptosis-modifying fusion protein is capable of binding a CC target cell and integrating into or crossing a cellular membrane of the CC target cell. The apoptosis-modifying fusion protein comprises at least CC two domains: the DTR domain, which targets the fusion protein to the CC target cell and the Bcl-XL domain, which modifies an apoptotic response CC inhibiting or enhancing) apoptosis in a target cell, such as neuron, CC lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or CC typer-proliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischaemic neuronal injury, CC especially spinal cord injury. The fusion protein may be used to treat CC of apoptosis in a subject after transient ischaemic neuronal injury, CC especially spinal cord injury. The fusion protein may be used to treat CC of apoptotic cellular response, including neurodegenerative disorders count as Alzheimer's disease, Huntington's disease, spinal muscular counters and counters. The apoptosis-modifying fusion protein can be delivered celfectively throughout the body and targeted to selective tissue and
       Sequence 1236 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 54-56; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAU00219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-AUG-2000; 2000WO-US22293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200112661-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-218343/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0149220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Linker DNA, linking Bcl-X1 to DTR" 778..1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= c
/note= "Bcl-xl gene from codon 1-233"
760..777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "10x Histidine tag 61..759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "DTR, diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Bcl-X1-DTR fusion protein"
       317 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "DTR is diphtheria toxin receptor binding domain"
291 C;
   343
G; 285
T; 0 other;
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alignment\_block:

Percent Similarity:

Quality: Ratio:

433.50 2.949 63.090

Percent Identity: 39.914

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seq_documentation_block:
ID AAH43464 standard; cDNA; 702 BP.
XX
AC AAH43464;
XX
DT 04-DEC-2001 (first entry)
XX
DE cDNA clone HP03564 ORF.
XX
KW Npw38; NpwBP; protein interaction;
KW localization; protein network; int
                                                                                                                                                                                                                                                                                                                            seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAS00247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-155-327E-7 x AAS00247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 CAGCAGTTTGGATGCCCGGGAGGTGATCCCCCATGGCAGCAGTAAAGCAAG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 AAGGGACTGAATCGGAGATGGAGACCCCCAGTGCCATCAATGGCAACCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 CAGCTGGAGTCAGTTTAGTGATGTGGAAGAACAGGACTGAGGCCCCAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 AGTGACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAG 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 CGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 CTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 laGluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArg 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 aTyrLeuGluThrArgLeuAlaAspTrpIleHisSerSerGlyGlyTrpA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526 GACAAGGAGGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 r..... 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 ArgAlaLeuValAlaAspPheValGlyTyrLysLeuArgGlnLysGlyTy 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 gPheThrGlnValSerAspGluLeuPheGlnGlyGlyProAsnTrpGlyA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe 61
     Npw38; NpwBP; protein interaction; reporter function; eukaryotic cell; localization; protein network; intracellular; primer; amplify; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGGAGCTGGTTGACTTTCTCTCCTACAAGCTTTCCCAGAAAGGATA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerAspLeuAlaAlaGlnLeuHisValThrProGlySerAlaGlnGlnAr 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....ProLeuHisGlnA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AsnLysGluMetGluProLeuValGlyGlnValGlnGluTrpMetValAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuArgGlu.....GlyAsnTrpAlaSerValArgThrValLeuThrGl 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                    yAlaValAlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaSer 192
                                                                                                                                                                                                                                                                                                                         /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH43464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of protein-protein interactions for screening compounds capable of modifying the interaction comprises observing intracellular localization of one protein after altering the modification pattern
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the open reading frame of the mitochondrial cDNA clone HP03564. The protein encoded by this sequence was used in the method of the invention. The method allows detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NISC-) JAPAN SCI & TECHNOLOGY
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166 TCCTGGCACCTGGCAGACAGCCCCGCGGTGAATGGAGCCACTGCGCACAG
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                                45 laMetArgAlaAlaGlyAspGluPheGluThrArgPheArgArgThrPhe
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                                                                     CAGCAGTTTGGATGCCCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAG
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OM of: US-09-155-327E-7 to: GenEmbl:*
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Query length: 193
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gb_om:SSJ001203
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582 i U59747 Human B.1-w (bc1-w) mRNI
1437 i Bc021198 Homo sapiens, BCL2-11
3542 i D87461 Human mRNA for KIAA0277
579 i AR020780 Sequence 2 from patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AR020780 Sequence 2 from patent
U59746 Mus musculus Bcl-w (bcl
AX022529 Sequence 6 from Patent
AX030817 Sequence 6 from Patent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY005131 Oryctolagus cuniculus
U51278 Mus musculus thymus Bcl
Ax085490 Sequence 1 from Paten
U26645 Gallus gallus bcl-x (bg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF030769 Mus musculus BCL-W ()
AR020779 Sequence 1 from paten
AF096291 Rattus norvegicus Bcl
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; ax345130 Sequence 201 from Pat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF216205 Sus scrofa anti-apopto
AJ001203 Sus scrofa mRNA for ar
                                                                                       U72350 Rattus norvegicus Bcl
                                                                                                                           AB073983 Canis familiaris mRNA
BD006625 A mutagenized rat bcl
           AF060226 Eukaryotic expression
                                               BC019307 Homo sapiens, clone
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gb_ro:RNCBLXLS
gb_ro:RNU10579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_om:BTU92434
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MEDLINE
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                                                                                                                                                                                                                                                                                 Quality: 1007.00
Ratio: 5.218
Percent Similarity: 100.000
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                                                                                                                                                                                     Align seg 1/1 to: HSU59747 from: 1 to: 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
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34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                             17
                                                                                                              TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                           eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S. bcl-w, a novel member of the bcl-2 family, promotes cell survival Oncogene 13 (4), 665-675 (1996) 96358615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Bcl-w (bcl-w) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U59747.1 GI:1572492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-JUN-1996) Molecular Biology Unit, The Walter an Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                         104
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GAALCAESVNKEMEPLYGQVGEWMYAYLGTRLADWIHSSGGWAEFTALYGDGALEEAR
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156 c 211 g 111 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="bcl-w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="promotes cell survival"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="bcl-w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428.50
424.50
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percent Identity: 100.000
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2.3e-27
1.7e-27
3.3e-27
1.8e-26
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1 U92434 Bos taurus bcl-2 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! Z11961 G.domesticus mRNA
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X82537 R.norvegicus bcl-x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 ACGAACTTTTTCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCTGACTGGATCCACAGCAGTGGGGGGGGCGGGGGTTCACAGCTCTA 450
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Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
                                                                                                  Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                           CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Cor DNA Sequencing by: National Institutes of i
                                                                                                                                                    DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC021198 1437 bp mRNA linear PRI 22-JAN-HOMO sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                          Consortium (LLNL)
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                                                      476 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 15 Row: k Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14574571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.
                      303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
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Align seg 1/1 to: BC021198 from: 1 to: 1437 Ratio: 5.218 Percent Similarity: 100.000 US-09-155-327E-7 x BC021198 Quality: 1007.00 Percent Identity: 100.000 Length:

- 17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34 1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
- 276 GGGAGGGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGCCAGCTGGA 34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
- 326 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 375
- nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
- 376 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 425
- 101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117 84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100 ATGAACTITTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 475
- 117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134

seq\_name: gb\_pr:D87461

seq\_documentation\_block:

D87461

DEFINITION

D87461

SOURCE KEYWORDS VERSION ACCESSION

KIAA0271

ORGANISM

Homo sapiens

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576 TGGCTGACTGGATCCACAGCAGTGGGGGGGGTTGGGGGGAGTTCACAGCTCTA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 palaservalargThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          626 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAACTGTAGGGGCCTTTTTTGCTAGCAAG 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGGCCCCTGG 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagase, T., Seki, N., Ishikawa, K., Ohira, M., Kawarabayasi, Y., Ohara, O., Tanaka, A., Kotani, H., Miyajima, N. and Nomura, N. Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mRNA for KIAA0271 gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens male brain myloblast cell_line:KG-1 cDNA to mrNA, clone_lib:pSPORT 1 clone:HA6752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D87461.1 GI:1944417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara, O., Nagase, T., Kikuno, R. and Nomura, N. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 3542)
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177. .758
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                                                                                817 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3542 bp
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US-09-155-327E-7 x D87461
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                                                                                                                                                                                                                                                        DEFINITION
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LOCUS AR020780
FEATURES
                                                                                                                                                                   SOURCE
                                                                                             REFERENCE
                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                    ACCESSION
                      JOURNAL
                                             TITLE
                                                                        AUTHORS
                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 ATGAACTTTTTCAAGGGGGCCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 GTCTTTGGGGCCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  677 GGCATCAGTGAGGACAGTGCTGACGGGGGCCCTGGCACTGGGGGCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 euAlaAspTrpIlcHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             627 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCTGACTGGATCCACAGCAGTGGGGGGGGTGGGCGGAGTTCACAGCTCTA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                        TAACTGTAGGGGCCTTTTTTGCTAGCAAG 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1007.00
Ratio: 5.218
                                                                                                                                                                                                                                  579 bp
Sequence 2 from patent US 5789201.
AR020780
                      Genes coding for bcl-y a bcl-2 homologue Patent: US 5789201-A 2 04-AUG-1998;
                                                                                                                                                                                                                AR020780.1 GI:3975395
                                                                        Guastella,J.
                                                                                                                                            Unknown
                                                                                                                                                                   Unknown
                                                                                                                   Unclassified
                                                                                             (bases 1 to 579)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526
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REFERENCE

JOURNAL TITLE AUTHORS JOURNAL MEDLINE

FEATURES

source

gene

CDS

(A24428)

PAT 05-DEC-1998

alignment\_scores:

ORIGIN BASE COUNT REFERENCE

TITLE AUTHORS

source

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ACCESSION
VERSION
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                                                                                                               seq_documentation_block:
LOCUS MMNTS4716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AR020780 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 5.219
Percent Similarity: 99.482
                                                                                                                                                                                                                   551 TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                       184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                 501 GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                       451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                                                              151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-155-327E-7 x AR020780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 GCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACCCAGGTCTCCG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GGGAGGCCCAGCAGCTGACCCACTGCACCAAGCCATGCGGGCAGCTGGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetalaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGAAGACTT 50
                                                                                                                                                                                                                                                                                                                           pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT
                                                                Mus musculus Bcl-w (bcl-w) mRNA, complete cds. U59746
                                         U59746.1 GI:1572494
house mouse
                                                                                                            MMU59746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 1002.00
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154 c 208 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 99.482
                                                                                                      582 bp
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                                                                                                        mRNA
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: MMU59746 from: 1 to: 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 100.000
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251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
                                                                                                                 201 GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
                                                                                                                                                                                                                            151 GACGAGTTTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                             34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
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                                                                                                                                                                                                                                                          AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 1000.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 582)
Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival
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17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                       1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes patent: EP 0932674-A 6 04-AUG-1999; AMRAD OPERATIONS PTY LTD (AU)
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Sequence 6 from Patent W09735971.
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Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
A novel mammallan gene, bcl-w, belongs to the bcl-2 family of
                                                                                                                                                                                                                                                                         apoptosis-controlling genes
Patent: WO 9735971-A 6 02-OCT-1997;
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ORIGIN
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   ORGANISM
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                                                                                                                                                                                                                         184 alThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                       451 TACGGGGACGGGCCCTGGAGGAGGCGCGCGTCTGCGGGAGGGGAACTG 500
                                                                                                                                                                                                                                                                                                                                                                      151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 CTCTTTGGGGCTGCACTGTGGTGCTGAGAGTGTCAACAAGGAGATGGAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                                                                                                                                                       TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                          GGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTGGGGGCCCCTGG
                                                                                                                                                                                                                                                                                                         pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTGGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCATGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA 150
Mus musculus
                                                  AF030769
AF030769.1 GI:2623249
                                                                                  Mus musculus BCL-W (Bcl-W) mRNA, complete cds.
                   house mouse
                                                                                                               AF030769
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Ratio: 5.181
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157 c 210 g 111 t
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                                                                                                         3476 bp
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alignment_block:
US-09-155-327E-7 x AF030769
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REFERENCE
AUTHORS
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                                                                                                                                                                                         Align seg 1/1 to: AF030769 from: 1 to: 3476
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JOURNAL
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229 TGTAGGCTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTG
                                                                             17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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Ratio: 5.181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 3476)
Ross, A.J. and MacGregor, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 3476)
ROSS,A.J., Waymire,K.G., MOSS,J.E., Parlow,A.F., Russell,L.D. and MacGregor,G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-OCT-1997) Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-w is required for testis homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                           /number=4
3356. 3364
3356. 3364
/gene="Bcl-w"
/note="mRNA destabilization element"
3428. 3441
/gene="Bcl-w"
1 /gene="Bcl-w"
1 814 c 991 g 875 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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171. .610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Bcl-w"
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/strain="C57BL/10J"
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                                                                                                                                                                                                                                                                  Percent Identity:
                                                                                                                                                                                                                                                                                                 Length:
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seq_documentation_block:
LOCUS AR020779
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                                                                                                                                                                                                                                                                                             REFERENCE
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                                                                           alignment_block:
US-09-155-327E-7 x AR020779
                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                      BASE COUNT
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                                                                                                           Ratio: 5.161
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                    TITLE
                                                 Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTGGGGGGCCCTGG
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Sequence 1 from patent US AR020779
                                                                                                                                                                                                                                         Genes coding for bcl-y a bcl-2 homologue Patent: US 5789201-A 1 04-AUG-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             AR020779.1 GI:3975394
                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                 Guastella,J.
                                                                                                                                                                                                                                                                                                                        Unknown
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                                                                                                                                                                                                                                                                                                           Unclassified.
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                                                    AR020779
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157 c 198 g
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                                                                                                                  Percent Identity: 98.446
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REFERENCE
AUTHORS
TITLE
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ACCESSION
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                                                                                                                                                                                                                          AUTHORS
                                                                               JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                        Hamner,S.; Skoglosa,Y. and Lindholm,D.
Differential expression of bcl-w and bcl-x messenger RNA in the
developing and adult rat nervous system
Neuroscience 91 (2), 673-684 (1999)
                                                                                                                                                                                                                                                                         Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                          AF096291.1 GI:3747129
                                                               University, Box 587, BMC,
                                                                             Submitted (01-OCT-1998) Developmental
                                                                                           Hamner,S., Skoglosa,Y. and Lindholm,D. Direct Submission
                                                                                                                                                                                                                                                                                                                             Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                              AF096291
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                                                                                                                                                                                                                                          (bases 1 to 582)
                                                                                                                            (bases 1 to 582)
/strain="Sprague-Dawley
             /organism="Rattus norvegicus"
                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            (bcl-w) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                            582 bp
                                                               Uppsala 751
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                                                                   Neuroscience, Uppsala
23, Sweden
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alignment_block:
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            501
                   167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                     451
                                                                                                            151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                               401 TGGCTGACTGGATCCACAGCAGTGGGGGGCTGGGCGGAGTTCACAGCTCTA 450
                                                                                                                                                                                                        134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGluPheThrAlaLeu 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
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GGCATCAGTGAGGACAGTGCTGACGGGGGCTGTGGCACTGGGGGCCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                  GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
                                                                                           TACGGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAGGGGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-155-327E-7 x AX022531
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251 ACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGCCGACCCCAGCCTCAACCCCAGACACACGCGCTCTAGTGGCTGACTT 50
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                      spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe
                                                                                         GCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAGGTTTCCG
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Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
A novel mammalian gene, bcl-w, belongs to the bcl-2
apoptosis-controlling genes
Patent: EP 0932674-A 8 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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GAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR
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seq_name: gb_pat:AX030819
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pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
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AX030819
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GAALCAESVNKEMEPLVGQVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 TGTAGGCTATAGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTGGTGGGACAAGTCCAGGATTGGATCGTGGCCTACCTGGAGACACGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGGGGACGGGCCTTGGAGGACGCACGGCGTCTTGCGGGAGGGCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLEUVALGIYGINVALGINGluTrpMctValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCC
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                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196292)

Hellig, R., Pettl, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Hellig, R., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Eckenberg, R., Brulls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Welssenbach, J. Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS0000B 196292 bp DNA linear PRI 22-MAY-
Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL049829.4 GI:8217859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL049829

    Web : www.genoscope.cns.fr)
    On Jun 3, 2000 this sequence version replaced gi:6138746
    ----- Genome Center

                                                                                    Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqrefégenoscope.cns.fr
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The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end): R-244E17 Downstream BAC (overlapping the SP6 end): C-2201G16 (AC=AL132855)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 2.0 Quality coverage: 7.94x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.genoscope.cns.fr/Contact: SeqRef@genoscope.cns.fr
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29
29
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69
89
                   dbSTS:STS18321
                                  RHdb: RH53698
                                                              Identified using the e-PCR software 128419. .128543
                                                                                                   dbSTS:STS25817
                                                                                                                   /note="matching EMBL:H22648
RHdb:RH53520
                                                                                                                                                                                 dbSTS:STS40201
                                                                                                                                                                                                                                  dbSTS:STS45044 Identified using the e-PCR software 107996. .108181
                                             /note="matching EMBL:R87257
                                                                                                                                                                                                     /note="matching EMBL:D11677
RHdb:RH47139
                                                                                                                                                                                                                                                                                       /note="matching EMBL:R94929
RHdb:RH65111
                                                                                                                                                                                                                                                                                                                   Identified using the e-PCR software 107758. .107951
                                                                                                                                                  128387. .128525
                                                                                                                                                             Identified using the e-PCR software
                                                                                                                                                                                                                                                                                                                                                     dbSTS:STS52191
                                                                                                                                                                                                                                                                                                                                                                                                                                       dbSTS:STS55514
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RHdb:RH102162
                                                                                                                                                                                                                                                                                                                                                                          RHdb:RH75103
                                                                                                                                                                                                                                                                                                                                                                                                          93580
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="matching EMBL:H79035 RHdb:RH78773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identified using the e-PCR software (G. Schuler)" 82164. .82299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dbsrs:srs68485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="matching EMBL:AA167748 RHdb:RH98727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identified using the e-PCR software (G. Schuler) 80433. .80566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dbsrs:srs69699
                                                                                                                                                                                                                                                                                                                                                                            93580. 93808
/note="matching EMBL:AA007328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="R-124D2"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e of bases with a quality value Location/Qualifiers
1. .196292
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/db_xref="taxon:9606"
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US-09-155-327E-7 x CNS0000B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: CNS0000B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                    90026 GCTGCATGTGACCCCAGGCTCAGCCCAACGACGTTCACCCAGGTCTCCG
                                                                                                                   89976 GATGAGTTCGAGACCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCA
                                                                                                                                                                                     89926 GGGAGGGCCCAGCAGCTGACCCGCTGCACCAAGCCATGCGGGCAGCTGGA
                                                                                                                                                                                                                                                     89876 TGTAGGTTATAAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCG
                                                                                                                                                                                                                                                                                                                      89826 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTT 89875
84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                          67
                                                                                                                                    51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STS
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                                                                                                                                                                                                        34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly
                                                                                                                                                                                                                                                                       17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
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                                                                                                                                                                                                                                                                                                                                       1 MetAlaThrProAlaSerAlaProAspThrArgAlaLeuValAlaAspPh 17
                                                                         nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
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dbSTS:STS53407
Identified using the e-PCR software
a 45673 c 47123 g 52626 t
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4.526
48.371
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RHdb:RH53972
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90076 ATGAACTTTTTCAAGGGGCCCCCAACTGGGGCCCGCCTTGTAGCCTTCTTT 90125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90376 AGTCTCCCCGTCTGGATGGAATTAGATTGAGAGATGCCTGGACTCTGCAC 90425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90276 GCCGCTCTGCACATCCTTCTGCAAAGCTGGTCTCCAGGGGGAAGATGGGG 90325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90576 TGGTGGTCAGGCAAGCCTTGGCAAAGGATGCTAGTTCTGAGCAGAATTTT 90625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90726 AGAAGAGCTTTGGCCAGAGAGGAGCTGGGTATGGGGTAGTGCTCGCAGTG 90775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90676 AGTCTCTCAGGGTGGGGGTGCACCTGGGGGGATCAGAGGGGGCTTGCAGGG 90725
                                                                                                                                                                                                                                                                                                         90826 GATATCCCTTCTCCTTCTTCTCTCCTGCTTCCCTTCTCTCCCACAGGC 90875
                                                                                                                                                                                                                                                                                                                                                                                                             90776 GATGGAACTGGAACTCTTCCTCTCCTCTTCTCCACTCTTTCCTCTCCT 90825
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                                                                                                90926 TGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCCCTG 90975
                                                                                                                                                                                                      90876 GGAGTTCACAGCTCTATACGGGGACGGGCCCTGGAGGAGGCGCGGCGTC 90925
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                                                                                                                                                                                                                                  146 .GluPheThrAlaLeuTyrGlyAspGlyAlaLeuGluGluAlaArgArgL 162
                                                                                                                                                                                                                                                                                                                                                        145 .....Ala 145
                                                 179 AlaLeuGlyAlaLeuValThrValGlyAlaPhePheAlaSerLys 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTTTACATCTGAGTCATGGCGTGGGGAGGTGGGGAGGACCAGGGATGGG 90575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euArgGluGlyAsnTrpAlaSerValArgThrValLeuThrGlyAlaVal 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
REFERENCE
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC079885 151212 bp DNA linear HTG 08-NO RATTUS norvegicus chromosome 4 clone RP31-246H18 strain Brown Norway, WORKING DRAFT SEQUENCE, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Ho,S.-L., Idol,J., Karlins,E., Lee-Lin,S.D., McCloskey,J.C.,
Maduro,O.L., Maduro,V.B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.
NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA on Nov 8, 2000 this sequence version replaced gi:10179358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC079885.2 GI:11120768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 147800 bases at least Q40 Consensus quality: 148726 bases at least Q20 Consensus quality: 149333 bases at least Q20 Insert size: 145000; agarose-fp Insert size: 150812; sum-of-contigs Quality coverage: 11.76x in Q20 bases; agarose-fp Quality coverage: 11.30x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 151212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 151212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                          20441
20541
41010
41110
65553
                              /strain="Brown Norway"
/db_xref="taxon:10116"
                                                                                  /organism="Rattus norvegicus"
                                                                                                           1. .151212
                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .--- project Information
                                                                                                                                                             20440: contig of 20440 bp in length 20540: gap of unknown length 41009: contig of 20469 bp in length 41109: gap of unknown length 65552: contig of 24443 bp in length 65652: gap of unknown length 110365: contig of 44713 bp in length 110465: gap of unknown length 151212: contig of 40747 bp in length.

    Summary Statistics

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alignment_scores:
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                                                         74915 TGGCTGACTGGATCCACAACAATGGGGGCTGGGTGGAGTTCACAGCTCTA 74964
                                                                                                                                                                                                                        74865 ATTGGTGGGACAAGTGCAGGATTGGATGGTGGCCTACCCCAGAGACACGCC 74914
                                                                                                                                                                                                                                                                                                        74815 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAGAAAAATAGAGCC 74864
                                                                                                                                                                                                                                                                                                                                                                                     74765 ACGAACTTTTCCAAGGGGCCCCAACTAGGGCCCATCTTGTGACATTCTTT 74814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74715 GCTACATGTGATGCCAGGCTCAGCCCAACAATGCTTCACCCAGGTTTCCA 74764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74665 GACAAGTTAGAGACCCCACTTCCAGCACACCTTCTCTGACCTGGCCACTCA 74714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74605 ......GCTGGCCCCG 74614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 pAlaSerValArgThrValLeuThrGlyAlaValAlaLeuGlyAlaLeuV 184
                                                                                                151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167
                                                                                                                                                                134 euAlaAspTrpIleHisSerSerGlyGlyTrpAlaGlupheThrAlaLeu 150
                                                                                                                                                                                                                                                117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
                                                                                                                                                                                                                                                                                                                             101 ValPheGlyAlaAlaLeuCysAlaGluSerValAsnLysGluMetGluPr 117
                                                                                                                                                                                                                                                                                                                                                                                                                           84 spGluLeuPheGlnGlyGlyProAsnTrpGlyArgLeuValAlaPhePhe 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 nLeuHisValThrProGlySerAlaGlnGlnArgPheThrGlnValSerA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 AspGluPheGluThrArgPheArgArgThrPheSerAspLeuAlaAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 lyGluGlyProAlaAlaAspProLeuHisGlnAlaMetArgAlaAlaGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 eValGlyTyrLysLeuArgGlnLysGlyTyrValCysGlyAlaGlyProG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGAAGGCCCAACAGCCAACCTGATACACCAAGCCATGTGGGCTGCTGGA 74664
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86.528
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110466. .151212
/note="assembly_fragment"
a 30838 c 31177 g 45417 t
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/note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP31-246H18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193
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FEATURES
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                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence. It currently * consists of 4 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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Bouffard, G.G., Brinkley, C., Dietrich, N.L., Gupta, J., Ho, S.-L.,
Idol, J., Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, Q.L.,
Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,
Pearson, R., Prasad, A., Snyder, B., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tran, J.T., Tsurgeon, C.,
Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.
NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                           as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0, 990319
Consensus quality: 179798 bases at least Q40
Consensus quality: 180132 bases at least Q20
Consensus quality: 180274 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 160000; pulse-field-gel
Insert size: 160982; sum-of-contigs
Quality coverage: 15.02x in Q20 bases; sugarose-fp
Quality coverage: 11.45x in Q20 bases; sum-of-contigs
Quality coverage: 11.45x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC084240.1 GI:10864175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: rl
Center clone name: 103L21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov
Location/Qualifiers
         5430: contig of 5430 bp in length 5530: gap of unknown length 39503: contig of 33973 bp in length 39603: gap of unknown length 85792: contig of 46189 bp in length 85892: gap of unknown length 181282: contig of 95390 bp in length.
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alignment_block:
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              151 TyrGlyAspGlyAlaLeuGluGluAlaArgArgLeuArgGluGlyAsnTr 167 ::: :::|||||||||||||||
                                                                                                                                       117 oLeuValGlyGlnValGlnGluTrpMetValAlaTyrLeuGluThrArgL 134
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/chromosome="4"
/clone="RP31-103L21"
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Perfect score:
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Maximum DB
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score greater than or equal to the score of the result being printed,
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6: /cgn2_6/ptodata/1
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first 45 summaries
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US-08-978-523-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (without alignments)
2161.129 Million cell updates/sec
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Sequence 16, Appl
Sequence 22, Appl
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Patent No. 5506344
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Sequence 8, Appli
Sequence 3, Appli
                                                                      Patent No.
Patent No.
Patent No.
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ALIGNMENTS

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Sequence 1, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Guastella, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-798-897-1
; MOLECULE TYPE: US-08-798-897-1
                                                                           TELEFAX: 202-3/1-2011
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                   TELEPHONE: 202-371-2600
                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                    TYPE:
                                                                                                                                                                                       NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: Februa
                                     TOPOLOGY:
                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   20005
                                                      nucleic acid
DEDNESS: both
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                                       both
                                                                                                                                                                                                                                                            February 11, 1997
N: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homologue
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                                                                                                                                                                                             1483.0140001
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Query Match Best Local Matches

Similarity

95.9%; 97.8%;

Score 558.2; DB 1; Pred. No. 2.3e-143; 0; Mismatches 13;

Length Indels

0; Gaps

0;

Conservative

0;

1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60

ATGGCGACCCCAGCCTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60

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            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                         ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Genes Cod:
TITLE OF INVENTION: HOMOLOgue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New 1
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                              APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
                                                                                                                                                                                APPLICATION NUMBER: US/08/978,523 FILING DATE: herewith CLASSIFICATION: 424
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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202-371-2540
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                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                          APPLICANT: Guastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y,
TITLE OF INVENTION: Homologue
                                                                                                                  NUMBER OF SEQUENCES: 5
                                                                                                                                                                              APPLICANT:
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TOPOLOGY: bot
MOLECULE TYPE:
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LENGTH: 579 base pairs
                                                                      STREET: 1100 New CITY: Washington
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                                                             STATE:
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                                              USA
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US-08-978-523-2
sequence 2, Application US/08978523
Patent No. 5883229
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; MOLECULE TYPE: cDNA US-08-798-897-2
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/798,897
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STRANDEDNESS: both
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REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                         241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                                                                                                                                                                                           241 caggtttccgacgaccttttccaagggggccctaactggggccgtcttgtggcattcttt 300
                                                                                                                      TOPOLOGY:
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                                                                            481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 88.5%; Score 515; DB 1; Length 579; Local Similarity 93.1%; Pred. No. 1.4e-131;
541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
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                                                             CGTCTGCCGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACTG 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Genes Cod:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Esmond, Robert W. REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: February 11, 1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/798,897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                         181 TICTCTGATCTGGCGGCTCAGCTGCATGTGACCCCCAGGCTCAGCCCAACAACGCTTCACC 240
                                                                                                                                                                                                                           181 ttototgacotggccgctcagctacacgtgaccccaggctcagcccaggctacacgcttcacc 240
                                                                                                                                                                                                                                                                             121
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361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
                                                                  301 GTCTTTGGGGCTGCACTGTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
                                                                                    301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
                                                                                                                                     241 CAGGTCTCCGATGAACTTTTTCAAGGGGGCCCCAACTGGGGCCGCCTTGTAGCCTTCTTT 300
                                                                                                                                                           241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                              61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC 120
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                                                                                                                                                                                                                                                                                                                                                                61 aggctgaggcagaagggttatgtctgtggagctggccctggggaaggcccagccgccgac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
                                                                                                                                                                                                                                                                                                                                                                                                                CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
248 ccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctttgtctttg 307
                                 454 ACCTGACATCCCACCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                    188 acctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacccaggttt 247
                                                                                               394 AGCAAGCGCTGAGGGAGGCGAGGCGACTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                  128 accaagccatgogggctgctggagacgagtttgagacccgttttccgccgcaccttctctg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene:
TITLE OF INVENTION: Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           Local
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REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 321 NC
CITY: Chicago
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58.3%;
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                                                                                                                                                                                Score 134.6; DB 1; Length 926; Pred. No. 8.7e-28;
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US-08-470-670A-6
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                                                                                                                                                      TELEFAX: (512) 474-75
INFORMATION FOR SEQ ID NO:
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                                                     FEATURE:
                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: AR TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                               NAME/KEY:
                                                                TOPOLOGY:
                                                                                    STRANDEDNESS:
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                                                                                                      TYPE:
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                                                                                                                                                                                                                                                                NAME:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 aggattggatggtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGGCCTTTTTCTCCCTTCG 573
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                                                                                                  nucleic acid
                                                                                                                                                                                                                                                         Highlander, Steven L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Houston
                                                                                                               926 base pairs
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                                                                                                                                                                      1: (512) 418-3000
(512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P.O. Box 4433
                                CDS
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                                                                   Linear
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Query Match Best Local Similarity

23.1%; 58.3%;

Score 134.6; DB 2 Pred. No. 8.7e-28; 0; Mismatches 169

DB 2; 169;

Length 926;

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Gaps

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Matches 236;

Conservative

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US-08-481-739-1
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Patent No. 6143291
GENERAL INFORMATION:
                                                                                                                                                                         TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: June, Carl H. and Thompson, Craig B.
TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: RP TELECOMMUNICATION INFORMATION: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        488 gggaggggaactgggcatcagtgaggacagtgctgacgggggccg 532
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                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07-JUNE PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
                                         FEATURE:
                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                               LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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  NAME/KEY:
                                                                              TOPOLOGY:
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135..836
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                                                            DNA (genomic)
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US-08-481-739-1
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                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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patent No. 6172216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nicholaf, Brian J.
APPLICANT: Stang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
                                                                             Matches
                                                                                                              Query Match
                                                                           Best Local Similarity Matches 236; Conserv
                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ISPH-0324
                                                                                                                                                                                                                                                                                                         LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                         FEATURE:
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128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
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Pred. No. 8.7e-28;
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APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
TITLE OF INVENTION: of mRNA Processing
FILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
EARLIER FILING DATE: 1998-10-07
EARLIER FILING DATE: 1998-10-07
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 39
LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
634 cagcttggatggccacttacctgaatgaccacctagagccttggatccaggagaacggcg 693
                                                                                                    368 aggattggatggtctacctggagacacgtctggctgactggattcacagcagtggcg 427
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Best Local Similarity
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SEQ ID NO 1
LENGTH: 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (135)..(836)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
DATABASE ENTRY DATE: 1994-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 09/277,020 EARLIER FILING DATE: 1998-03-26 EARLIER APPLICATION NUMBER: 09/167,921 EARLIER FILING DATE: 1998-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Nickoloff, Brian J. APPLICANT: Zhang, QingQing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bennett, C. Frank APPLICANT: Dean, Nicholas M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ISPH-0368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Monia, Brett P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
754 aggaacgcttcaaccgctggttcctgacgggcatgactgtggccg 798
                              488 999a9999aactg99catca9tgaggacagtgctgacgggggccg 532
                                                                                    694 gctgggatacttttgtggaactctatgggaacaatgcagcagccgagagccgaaagggcc
                                                                                                                                                                              634 cagcttggatggccacttacctgaatgaccacctagagccttggatccaggagaacggcg
                                                                                                                                                                                                        368 aggattggatggtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
                                                                                                                                                                                                                                                                   574 gcggggcactgtgcgtggaaagcgtagacaaggagatgcaggtattggtgagtcggatcg 633
                                                                                                                                                                                                                                                                                               308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtgc 367
                                                                                                                                                                                                                                                                                                                                                        514 tgaatgaactcttccgggatggggtaaactggggtcgcattgtggcctttttctccttcg 573
                                                                                                                                                                                                                                                                                                                                                                                    248 ccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctttgtctttg 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 accaagccatgogggctgctggagacgagtttgagacccgttttccgccgcacctttctctg 187
                                                                                                                                                                                                                                                                                                                                                                                                                                               454 acctgacatcccagctccacatcaccccagggacagcatatcagagctttgaacaggtag
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                                                                                                                                 9ct999c99agttcacagctctatacggggacggggccctggaggaggcacggcgtctgc 487
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58.3%;
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US-08-461-511A-6
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                                                                                                                                                                                                                                                                                                                             454 ACCTGACATCCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                                                                                                                                                      308 gggctgcctgtgtgctgagagtgtcaaccaaagaaattggagcctttggtgggacaagtgc 367
                                                                                                                                                                                                                                               514 TGAATGAACTCTTCCGGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573
694 GCTGGGATACTTTTGTGGAACTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753
                                    428 gctgggcggagttcacagctctatacggggacggggccctggaggaggcacggcgtctgc 487
                                                                              634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 693
                                                                                                                   368 aggattggatggtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
                                                                                                                                                              574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633
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Boise, Lawrence H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A
EPILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 135..836
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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REFERENCE/DOCKET NUMBER: ARCD:179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/08:
FILING DATE: 22 JUNE 1993
ATTORNEY/AGENT INFORMATION:
NAME: PARKER, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DC
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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ZIP: 77210
                                                                                                                                                                                                                                                         128 accaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcaccttctctg 187
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                                                                                                                                                                   454 ACCTGACATCCCAGCTCCACATCACCCCAGGGACAGCATATCAGAGCTTTGAACAGGTAG 513
                                                                                                                                                                                       188 acctggccgctcagctacacgtgaccccaggctcagcccaggcaacgcttcacccaggttt 247
                                                                                                                                                                                                                                    394 AGCAAGCGCTGAGGGAGGCAGGCGACGAGTTTGAACTGCGGTACCGGCGGGCATTCAGTG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                    514 TGAATGAACTCTTCCCGGATGGGGTAAACTGGGGTCGCATTGTGGCCTTTTTCTCCTTCG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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368 aggattggatggtggcctacctggagacacgtctggctgactggatccacagcagtggcg 427
                                    574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGAGTCGGATCG 633
                                                               308 gggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtgc 367
                                                                                                                     248 ccgacgtacttttccaagggggccttaactggggccgtcttgtggcattctttgtctttg 307
                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                                                                                                                           236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS, ASCII
                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          135..836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                           23.1%; 58.3%;
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                                                                                                                                                                                                                                                                                                             0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                           Score 134.6; DB 5; Length 926; Pred. No. 8.7e-28;
                                                                                                                                                                                                                                                                                                                  Indels
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US-08-465-485A-20
                                                                                Matches
                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                   TELEFAX: (408) 436-207 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                           MOLECULE TYPE: FEATURE:
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244 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGGCCAAGCCGGC 303
                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 20-SEP-1993 PRIOR APPLICATION DATA:
                    91 getggecetggggaaggecegecegecegetgeaceagecatgegggetgetgga 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Regulation of bcl-2 Gene Expression NUMBER OF SEQUENCES: 29
                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fortney, Andrew D. REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 21-FEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1755 S. CITY: Arlington STATE: Virginia
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STREET: 1755 S. Jefferson Davis Hwy., Suite 400
                                                                              213;
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                                                                                                                                                                                                                                                                  nucleic acid
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                                                                           Conservative
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                                                                                                                                                                                                                  DNA (genomic)
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                                                                                20.9%; Score 121.8; DB 2; Length 717; 58.4%; Pred. No. 2.5e-24;
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 Mismatches

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US-09-080-285-20
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                               TELEFAX: (408) 436-20 INFORMATION FOR SEQ ID NO:
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Patent No. 6
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SEQUENCE CHARACTERISTICS:
LENGTH: 717 base pairs
                                                                              REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
                                                                                                                                               FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                               FILING DATE: 21-FEB-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: US 07/840,716
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 29
                                                                    TELEPHONE:
                                                                                                                                        NAME:
                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 22202
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                                                                                                                                  Fortney, Andrew D.
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1755 S. Jefferson Davis Hwy., Suite 400
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                                                (408) 436-2070
108) 436-2075
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                                                                                                                                                                                                               21-FEB-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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US-08-470-670A-1
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Best Local Similarity
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Patent No. 5834309
Patent No. 5834309 5710045
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                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thompson, Craig B. B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,448
FILING DATE: 22-JUN-1993
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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LOCATION:
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STRANDEDNESS: single
TOPOLOGY: linear
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CITY: F
STATE:
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ZIP: 77210
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                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                      Houston
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                                                                                                                                                                                                                                                     Texas
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                                                                                        US/08/470,670A
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TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARE TELECOMMUNICATION INFORMATION:
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NAME: Highlander, Steven L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                           483 GCGACCTCACCTCCAGCTCCACATCACCCCTGGCACGGCGTACCAGAGCTTTGAGCAGG 542
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                                                                                                                                                                                                                                543 TAGTGAATGAACTCTTCCATGATGGTGTGAACTGGGGGCGCGTTCGTGGCTTTCTTCTCCT 602
                                                                                                                                                                                                                                                    245 tttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctttgtct 304
                                                                         663 TTGTGTCTTGGATGACCACGTACTTGACCGACCATCTAGATCCCTGGATCCAGGAGAATG 722
                                                                                                                                                    603 TCGGAGGGGCTTTGTGCGTGGAGAGCGTGGACAAGGAGATGCGGGTACTGGTGGGACGCA 662
                                                                                                                                                                           305 ttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgggacaag 364
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ALIGNMENTS

RESULT AK015644 DEFINITION SOURCE VERSION ACCESSION REFERENCE KEYWORDS Locus REFERENCE REFERENCE ORGANISM TITLE AUTHORS MEDLINE JOURNAL TITLE AUTHORS MEDLINE JOURNAL TITLE AUTHORS JOURNAL MEDIINE PUBMED PUBMED Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,K., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Vazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer genome Res. 10 (11), 1757-1771 (2000) AK015644 1949 bp mRNA linear HTC 19-JAN-Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930488D08:Bcl2-like 2, full insert sequence. Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) Mus musculus (strain:C57BL/6J) adult male t clone\_lib:RIKEN full-length enriched mouse Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mus musculus clone:4930488D08. HTC; CAP trapper AK015644.1 GI:12854052 99279253 11042159 20499374 0349636 (sites) (sites) (sites) male testis cDNA to mRNA, CDNA library HTC 19-JAN-2002

Query Match

Local

Similarity

99.5%; 99.7%;

Score 578.8; DB 11 Pred. No. 4.6e-132;

DB 11;

Length 1949;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to
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                                                                                                                                                   Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                   3487 bp mRNA linear HTC 19-JA Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200009L24:Bcl2-like 2, full insert command AK004680
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The RIKEN Genome Exploration Research Group Phase II Team and the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                       /gene="Bcl212"
209. .790
                                                                                                                                     /tissue_type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
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/clone="1200009L24"
                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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/note="Bcl2-like 2
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                                                                                                DKFZP761D0816_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZP761D0816 5', mRNA sequence.
                Homo sapiens
                                                                                                                                     AL157542
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                     AL157542.1
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/db_xref="GI:12836028"
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541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
                                                                481 cytctycygyaaggygaactygycatcaytyaggacagtyctyacgygygccytggcacty 540
                                                                                                                          554 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGAC-GGGCCCTGGAGGAGGCGCGG
                                                                                                                                                                                                          361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
                                                                                                                                                                                                                                                                                                            434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 193
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                                                                                                                                                  agt9gc9gct9ggcg9agttcacagctctatacggggacgggggccctggaggaggcacgg
                                            CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCCGTGGCACT-
                                                                                                                                                                                                                                                                                            GTCTTTGGGGCTGCACTGTGTGCNGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 493
                                                                                                                                                                                                                                                                                                                       9tctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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This clone (DKFZp761D0816) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Am Klopferspitz 18a D-82152 Martinsried, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 804)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.
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217 c 294 g 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="DKFZp761D0816"
/clone_lib="761 (synonym: hamy2)"
/tissue_type="amygdala"
/dev_stage="adult"
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142 t 1 others
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241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt 300
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                                                                                                                                                                                                                                                                                                                                          1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
                                            TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC
                                                                         ttctctgaccttggccgctcagctcacacgtgaccccaggctcagcccagcaccagcaacgcttcacc
                                                                                                                                                                | 0090t90accaa90cat90g9g0t90t9gagacgagtttgag9acccgtttccgccgcacc 180
                                                                                                                                                                                                                           AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
                                                                                                                                      CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                   528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: image.llnl. Plate: LLCM800 row: p column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 5 High quality sequence stop: 709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DHIOB (phage-resistant)"
//note="Organ: lung; Vector: pOTBF; Site_1: XhoI; Site_2: FOORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubbn (University of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Stratagene) and Superscript II RT (Life Technologies)."
284 c 386 g 170 t
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/clone="IMAGB:3944307"
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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90.7%;
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Pred. No. 1.1e-111;
0; Mismatches 54;
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COMMENT

FEATURES

REFERENCE

TITLE AUTHORS SOURCE KEYWORDS VERSION

ORGANISM

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21 cccagacacacgggctctagtggctgactttgtaggctataggctgaggcagaagggtta 80
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BASE COUNT
ORIGIN
                                                Query Match
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                     Matches 530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481. cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 815)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence start: 3 quality sequence stop: 650.
                              Conservative
                                                                                                                                                                                        /db_xref="taxon:10090"
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/clone=\normalfont NGER-Kid14"
/clone=\normalfont NGER-Kid14"
/note=\normalfont Nger \normalfont Nger \normalf
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                      76.5%;
96.5%;
                                                      pred. No. 3e-99;
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                                    Mismatches
                                                                                    DB 10; Length 815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GGCTGCTGGAGACGAG-TTGAGACCCGTTTCCGCCGCACCTTCTCTGACCTGGCCGCTCA 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 tgctgagagtgtcaacaaagaaatggagcctttggtgggacaagtgcaggattggatggt 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI1526 row: k column: 15
                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                 High quality sequence start: 21 High quality sequence stop: 695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                         Location/Qualifiers
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mRNA

linear

EST 25-SEP-2001

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KEYWORDS
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                                   Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA
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          lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site-1: NotI; Site-2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
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                                                                                                           Rot = 37.5. Second strand cDNA was prepared with the primer of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JUL-2000) roshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Fax:81-45-503-9216)
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High-efficiency full-length cDNA cloning
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                                                                                                                                                                      agtggcggctggg 433
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                                                      602396527F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511215
BG298789.1 GI:13063794 EST.
                           BG298789
                                         mRNA sequence
                                                                       BG298789
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/db_xref="GI:12850488"
/db_xref="GI:12850488"
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/translation="MATPASTPDTRALVADFVGYKLROKGYVCGAGPGEGPAKDPLHQ
AMRAAGDEFETRFRTFSDLAAOLHVTPGSAQORFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWVRSSQLLLSASLYKVG
LHGKIGPLMGGWGCAGRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="BCl212"
196. .732
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/note="Bcl2-like 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="10, 11 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="MGD:MGI:1902183"
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Pred. No. 1.7e-95;
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                                421 agtggcggctgggcgga 437
                                                                         458 CAAGTGCAGGATTGGATGGCCGTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
                                                                                                                                                                                        301
518 AGTGGGGGCTGGTAAGA 534
                                                                                                              361
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                                                                                                                                                 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA
                                                                                                                                                                                                                                                 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt
                                                                                                                                                                                                                                                                                                      TTCTCTGACCTGG-CGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
                                                                                                                                                                                                                                                                                                                          ttototgacotggccgctcagctacacgtgacoccaggctcagcccagcaacgcttcacc
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                                                                                            caagtgcaggattggatggttggcctacctggagacacgtctggctgactggatccacagc 420
                                                                                                                                                                     gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgga
                                                                                                                                                                                                                            CAGGTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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/clone_lib="NII_""".
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: eye; Vector: pCMV-SPORT6; Site_2" all; Cloned unidirectionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Note: this is a NIH_MGC Library."
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98.6%;
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Pred. No. 2.4e-92;
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VERSION
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                                                                                                                                                                      121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                        172 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCCAGCCGCCGAC 231
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                                                                                                  61 aggctgaggcagaagggttatgtctgtggagctggccctgggggaaggcccagccggcc 120
                                                                                                                                                                                                                                                                                                           TOCGI
425;
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW258BLU 540 bp mRNA linear EST 23-I um74a02.yl Sugano mouse kidney mkia Mus musculus CDNA clone IMAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS REGULATOR BCL-W. [2] SW:BCLW_MOUSE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             //dev_staye-_____/lab_host="DHIOB"
//lab_host="DHIOB"
//note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
//note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
//note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
//note="Organ: kidney; Vector: pME18S-FL3; Site pme18; PME18S-FL3; Signated to a DraIII adaptor [TGTTGGCCTATGG], digested and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Traffithte of Medical Science). Custom primers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer: custom primer used
                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:2300906"
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98.8%;
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Pred. No. 4.5e-91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 643.
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Plate: LLAM11548 row: j column: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 643)

NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institutes of Health, Mammalian Gene Collection (MGC)
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                1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NH_MCC Library."
                                                                                                                                                                                            /Clone="lib="NIH_MGC_118"
/Clone=lib="NIH_MGC_118"
/Clone=lib="NIH_MGC_118"
/Lissue_type="leukocyte"
/Lib_host="DH10B"
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Query Match

Best Local Similarity

63.0%;

Score 366.8; DB Pred. No. 5e-80;

DB 10;

Length 643;

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                                                                                                                                                                                                                                                                                                                                                                                            Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA596919.1 GI:2412354
                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nouse mouse
                                                                                     High quality sequence stop: 334
                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases
                                                                                                              primer: -28m13 rev2 ET from Amersham
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/db_xref="taxon:10090"
              /strain="C3H"
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                                                                                                                                                                                                                                                                                                                                                                                               603050701F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190792 5',
                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@nail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                 Luxalyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 758)
                                                                                                                                                                                                                                                                                                                                             BI764428.1 GI:15756006
                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                       BI764428
DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                     National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pf7T3D-Pac (Pharmacia) with a modified /note="Vector: pf7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', representation of the primer formacian stranded cDNA was ligated to Eco RI adaptors 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pf7T3 vector. Not I and Eco RI sites of the modified pf7T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates (available from ATCC) catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           characteristic muscle proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
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Pred. No. 6.6e-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 gtctttggggctgccctgtgtgctgagagtgtcaacaa 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccaggcaacgcttcacc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 198
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Ishii Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.
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                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                            BBB55021 RIKEN full-length enriched, B16 F10Y cells Mus musculus CDNA clone G370030007 5', mRNA sequence.
                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                nouse mouse
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                                                                                                                                                                                           (bases 1 to 457)
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pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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/clone="IMAGE:5190792"
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90.5%;
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                                                                                                                                                                                                        Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
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                           301 gtctttggggctgcc 315
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                                                                                          384 CAGGTTT-CGACGAACTTTT-CAAGGGGGCCCTAACTGGGGCCGTC-TGTGGCATTCTTT
                                                                                                                        241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt 300
                                                                                                                                                                                                                      181 ttctctgacctggccgctcaggctacacgtgaccccaggctcagcccagcagcgctcacc
                                                                                                                                                                                                                                                                                                   264 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGGCGCACC
                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                         204 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCAGCCGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 ATGGCGACCCCAGCCTCAACCCCAGACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
                                                                                                                                                                                                                                                                                                                                            ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-45-503-9216
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/clone="6370030007"
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154 c 137 g 85 t
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/strain="C57BL/6J"
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1. .457
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98.78;
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Pred. No. 4.6e-58;
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Best Local
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                                                                                                                     241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctt 299
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                                                                                                                                                                                                                                              246 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                                                                                                                                                                                                                                                   186 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG677345 749 bp mRNA linear EST 01-MAY-2001
602624059F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748943 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 749)
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BF204905 601 bp mkNA linear Est of No. 101 bp mkNA linear Est of No. 101866718F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="squamous cell carcinoma"
/tlab_host="DH10B (T1 phage-resistant)"
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/note="organ: skin; Vector: pCvV-SPORT6; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 239 c 219 g 135 t
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/clone_lib="NCI_CGAP_Skn4"
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90.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           524 CAAGTGCAGGAGTGGATGGTGGCTACTGTGAGACGCGGTCTGGCTGATCTGGATCCAAAG 583
                                                  361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
                                                                                                                                                                                                                        301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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                                                                                                                                                                                                                                                                                                                                                                                                   242 aggtttccgacgaact-tttccaagggggcccttaactggggccgtcttgttggcattcttt 300
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Tissue Procurement: ATCC
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Plate: LLCM987 row: d column: 05
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/clone_lib="NHH_MGC_17"
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/lab_Nost="DH10B (phage-resistant)"
/lab_Nost="DH10B (phage-resistant)
/lab_Nost="DH10B (phage-resistant)"
/la
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81.7%;
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Pred. No. 1.7e-50;
"'amatches 72;
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Search completed: June 6, 2002, 11:24:34 Job time: 5590 sec

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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                               June 6, 2002, 11:58:14; Search time 1853.13 Seconds (without alignments) 6572.256 Million cell updates/sec
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## ALIGNMENTS

TITLE JOURNAL	MEDLINE REFERENCE AUTHORS	TITLE	REFERENCE	ORGANISM	KEYWORDS SOURCE	ACCESSION VERSION	2	RESULT 1
Cory,S. Direct Submission Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne	96358615 2 (bases 1 to 582) Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and	Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival oncogene 13 (4), 665-675 (1996)	1 (bases 1 to 582) Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G.,	Mus muscullus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	house mouse.	U59746.1 GI:1572494	MMU59746 582 bp mRNA linear ROD 29-SEP-1996	

Result No.

Score

Query Match Length DB

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Description

SUMMARIES

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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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3476 bp
BCL-W (Bcl-w) mRNA,
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99.7%;
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Pred. No. 6e-125;
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Local Similarity
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                   ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgttttccgccgcacc
                                                                                                     aggotgaggcagaagggttatgtotgtggagotggcoctggggaagggoccagccggccgac 120
CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 3476)
1 (bases 1 to 3476)
Ross, A.J., Waymire, K.G., Moss, J.E., Parlow, A.F., Russell, L.D. and
MacGregor, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University, 1462 Clifton Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-OCT-1997) Center
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Ross, A.J. and MacGregor, G.R.
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3428. 3441
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/strain="C57BL/10J"
/db_xref="taxon:10090"
/chromosome="14"
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Pred. No. 4.9e-125;
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                                                                                                                                                                Hamner,S., Skoglosa,Y. and Lindholm,D.
Differential expression of bcl-w and bcl-x
developing and adult rat nervous system
Neuroscience 91 (2), 673-684 (1999)
                                                                                                                   Direct Submission
                                                                                                                            2 (bases 1 to 582)
Hamner,S., Skoglosa,Y. and Lindholm,D.
                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                 Rattus norvegicus
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                                                                                                                                                                                                                                                                                                   norvegicus Bcl-w
                          /dev_
                                   /strain="Sprague-Dawley
/db_xref="taxon:10116"
/tissue_type="brain"
       /gene="bcl-w"
                                                             /organism="Rattus norvegicus"
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                GI:3747129
                         _stage="postnatal"
                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                             Neuroscience,
23, Sweden
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AR020779 .
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/protein_id="AAC64200.1"
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GAALCAESVNKEMEPLVGQVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEAR
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                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)

1 (bases 1 to 582)

1 (bases 1 to 582)

2 (bases, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G., Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S. bcl-w, a novel member of the bcl-2 family, promotes cell survival 96358615

96358615
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Gibson,L., Holmgreen,S.P.,
Cory,S.
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                                                              CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACTG
                                                                              cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
                                                                                                                                           agtggcggctgggcggagttcacagctctatacggggacggggccctggaggaggaggcacgg 480
                                                                                                                                                                                                       caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc
                          ggggccctggtaactgtaggggccttttttgctagcaagtga 582
                                                                                                                            AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCCTGGAGGAGGCGCGG
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/protein_id="AAB09055.1"
/protein_id="AAB09055.1"
/db_xref="GI:1572493"
/db_xref="GI:1572493"
/translation="MARPASAPDTRALYADFVGYKLROKGYVCGAGPGEGPAADPLHQ
/translation="MARPASAPDTRALYADFVGYCGAGPGEGPANGRIVAFFVF
AMRAAGDEFETRFRTFSDLAAOLHVPGSAOQRFTOYSDELFQGGPANGRIVAFFVF
AAACAAESVNKEMEPLVGGVGEMAVAYLETRLADMIHSSGGWAEFTALYGDGALEEAR
RLREGSWASVRTVLTGAAALGALVTVGAFFASK"

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241 caggtttccgacgaacttttccaagggggccctaactggggccgtcttgtggcattcttt 300
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                                                                                                                                    121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                           237
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                                                                                                                                                                                                                                                                                              1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
                                      TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC
                                                            ttetetgaeetggeegeteagetaeaegtgaeeeeaggeteageeeageaaegetteaee 240
                                                                                                               CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 356
                                                                                                                                                                                            AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC 296
                                                                                                                                                                                                                   aggctgaggcagaagggttatgtctgtggagctggccctggggaaggcccagccgccgac 120
                                                                                                                                                                                                                                                                        ATGGCGACCCCAGCCTCGGCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 236
                                                                                                                                                                                                                                                                                                                                                               544;
                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohara,O., Nagase,T., Kikuno,R. and Nomura,N. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 3542)
Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y.,
Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.
Prediction of the coding sequences of unidentified human genes, VI.
The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced by analysis of cDNA clones from cell line KG-1 and brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 3 (5), 321-329 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens male brain myloblast cell_line:KG-1 cDNA to clone_lib:pSPORT 1 clone:HA6752.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="Baa19666.1"
//db_xref="GI:1944418"
//db_xref="GI:1944418"
//tzanslation="Matpasapdtralvadevgyklrokgyvcgagpgegpaadplho
amraagdefetrerrtesdlaaglhvypesaagoretgysdelfoggpnwgrlvaffvf
gaalcarsvnkemeplvgoyoewmvayletrladwihssggwabetalygdgaleear
glregnwasvrtvltgavalgalytvgaffask"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="myloblast"
/tissue_type="brain"
/clone_lib="pSPORT 1"
177. .758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to human transforming protein bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="KIAA0271"
177. .758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell
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                                                                                         61 aggctgaggcagaagggttatgtctgtggagctggccctgggggaaggcccagccggcc 120
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                                                                                                                                       1 ATGCCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
                                                                                                                                                            1 atggcgaccccagcctcaacccccagacacacgggctctagtggcttgactttgtaggctat 60
                                                                                                                                                                                                                                      Local Similarity
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                    ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                    AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
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Patent: EP 0932674-A 6 04-AUG-1999;
AMRAD OPERATIONS PTY LTD (AU)
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/Godon_start=1
/protein_id="CAC07880.1"
/db_xref="G1:10046126"
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                                            ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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Sequence 6 from Patent WO9735971.
AX030817
                                                                                                      543;
                                                                                                                                                                                                                                                                                                                                                                                                                       Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes patent: WO 9735971-A 6 02-CCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified
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                                                                                                                                                                                                                                                                                                                                                                                             ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU) ; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
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Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
                     Contact:

nisc_mgc@nhgri.nih.gov
Contact:
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Bakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Karlins,E., Legaspi.R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi.R.,
Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Walker,M.A.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                  CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                 Web site:
                                                                                                                                                                              Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                              Institute,
Zhang, L.-H. and Green, E.D.
                   Tiongson, E.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 1437)
                                                                                                                                                                                                                                                                                                                                                                                              31 Center Drive, Room 11A03, Bethesda,
                                                                                                                                                                 http://www.nisc.nih.gov/
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14574571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303
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/product_BCL2-like 2"
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/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
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/db_xref="LocusID:599"
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1. .1437
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              Rattus norvegicus chromosome 4 clone RP31-246H18 si
Norway, WORKING DRAFT SEQUENCE, 5 unordered pieces
ACO79885
AC079885.2 GI:11120768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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                 misc_feature
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Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Ho,S.-L., Idol,J., Karlins,E., Lee-Lin,S.-Q., Legaspi,R., Lim,M.,
Maduro,Q.L., Mastrian,S.D., McCloskey,J.C.,
Maduro,Q.L., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W.,
Thomas,J.W., Thomas,P.J., Walker,M.A., Wetherby,K.D. and Green,E.D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA on Nov 8, 2000 this sequence version replaced gi:10179358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid: n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: Dye-terminator Big Dye; 900319
Assembly program: Phrap; version 0.990319
Consensus quality: 147800 bases at least Q40
Consensus quality: 148726 bases at least Q30
Consensus quality: 149333 bases at least Q20
Consensus quality: 149333 bases at least Q20
Insert size: 145000; agarose-fp
Insert size: 150812; sum-of-contigs
Quality coverage: 11.76x in Q20 bases; sum-of-contigs
Quality coverage: 11.30x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                       20441
20541
41010
41110
65553
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                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/strain="Brown Norway"
                    vector_side:right"
20541. .41009
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                       /db_xref="taxon:10116"
/note="assembly_fragment
                                                                                                                                                         /clone_lib="RP31"
                                                                                                                                                                                                                                                                                                                                                                      20440: contig of 20440 bp in length 20540: gap of unknown length 4109: contig of 20469 bp in length 41109: gap of unknown length 6552: contig of 24443 bp in length 65652: gap of unknown length 110365: contig of 44713 bp in length 110465: gap of unknown length 151212: contig of 40747 bp in length.
                                                                                                          /note="assembly_fragment
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BASE COUNT
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Best Local 9
                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                              AC084240
                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                               KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74581 AGACACATEGGCTCTAATGGTTGAGCTGGCCCCGGGGAAGGCCCAACACCAACCTGATA 74640
                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74701 GACCTGGCCACTCAGCTACATGTGATGCCAGGCTCAGCCCAACAATGCTTCACCCAGGTT 74760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74641 CACCAAGCCATGTGGGCTGCTGGAGACAAGTTAGAGACCCACTTCCAGCACACCTTCTCT 74700
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                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74761 TCCAACGAACTTTTCCAAGGGGCCCCAACTAGGGCCATCTTGTGACATTCTTTGTCTTT 74820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75061 CTGATAACTGTAAGGGCCTTTTTTACTAACAAGTAA 75096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74941 GGCTGGGTGGAGTTCACAGCTCTATTCCGGAATGGGGCCCTAGAAGAGACATGGTGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 caccaagccatgcgggctgctggagacgagtttgagacccgttttccgccgcgcaccttctct 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 tccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctttgtcttt 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 aggcagaagggttatgtotgtgggagctggccctggggaaggcccagccgccgccgacccgctg 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 ggctgggcggagttcacagctctatacggggacggggccctggaggaggcacggcgtctg 486
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43370 a 30838 c 31177 g 45417 t
                                                                                                                                                                                                                                                                                                                                      ACO84240 181282 bp DNA linear HTG 18-OC7
Rattus norvegicus chromosome 4 clone RP31-103L21 strain Brown
Norway, WORKING DRAFT SEQUENCE, 4 unordered pieces.
lichases 1 to 181282)

1 (bases 1 to 181282)

Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,

Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,

Beckstrom-Sternberg, S.M., Lim, M.L., Gupta, J., Ho,S.-L.,

Bouffard, G.G., Brinkley, C., Dietrich, N.L., Gupta, J., Ho,S.-L.,

Bouffard, G.G., Brinkley, C., Dietrich, N.L., Maduro, Q.L.,

Bouffard, G.G., Brinkley, C., Dietrich, N.L., Maduro, Q.L.,

Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J.,

Pearson, R., Prasad, A., Snyder, B., Stantripop, S., Thomas, J.W.,

Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tran, J.T., Tsurgeon, C.,
                                                                                                                                                                                                                     Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                       AC084240.1 GI:10864175
                                                                                                                                                                                                                                                                                                              AC084240
                                                                                                                                                                                                                                                                                                                                 Norway, WORKING DRAFT SEQUENCE,
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 8.7e-85
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BASE COUNT
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                      Matches
                                    Dest Local Similarity 86.68;
                                                          Query Match
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AUTHORS
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                      447;
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                                                                                                                                                50811 a
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Submitted (18-OCT-2000) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vogt.J.L., Walker,M.A., Wetherby,K.D. and Green,E.D. NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319

Consensus quality: 17979% bases at least Q40

Consensus quality: 180132 bases at least Q30

Consensus quality: 180274 bases at least Q30

Insert size: 138000; agarose-fp
Insert size: 138000; pulse-field-gel
Insert size: 160000; pulse-field-gel
Insert size: 180982; sum-of-contigs

Quality coverage: 15.02x in Q20 bases; sqarose-fp
Quality coverage: 12.95x in Q20 bases; sum-of-contigs

Quality coverage: 11.45x in Q20 bases; sum-of-contigs
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2 (bases 1
               Conservative
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5531
39504
39604
85793
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Center clone name: 1031
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Contact: nisc_mouse@nhgri.nih.gov
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85893. 181282
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a 36290 c 37296 g 56560
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP31-103L21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5430: contig of 5430 bp in length
5530: gap of unknown length
39503: contig of 33973 bp in length
39603: gap of unknown length
85792: contig of 46189 bp in length
85892: gap of unknown length
181282: contig of 95390 bp in length.
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                                                                                                                                                                                                                             .85792
           0; Mismatches
                        Score 405.6; DB 2
Pred. No. 8.6e-85;
                                                                                                                                     56560 t
                                                 DB 2;
         69;
                                                                                                                                  325 others
    Indels
                                          Length 181282;
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  The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end) : R-244E17

Downstream BAC (overlapping the SP6 end) : C-2201G16 (AC-AL132855)
                                                                                                                                                                                             Submitted (21-MAY-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Jun 3, 2000 this sequence version replaced gi:6138746.
                                                                                                                                                             Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 196292)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Sequencing of the human chromosome 14
                                                                                                  Contact: SeqRef@genoscope.cns.fr
                                                                                                                                Web site:
                                                                                                                                                    Center code: GS
                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNSO000B 196292 bp DNA linear PRI 22-MAY-HUMAN chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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----- Summary Statistics
                                                                                                                      http://www.genoscope.cns.fr/
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/note="matching EMBL:H79035
RHdb:RH78773
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RHdb:RH98727
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/db_xref="taxon:9606"
/chromosome="14"
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RHdb:RH65111
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                                                                                                                                                                         Identified using the e-PCR software 128387. .128525
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/note="matching EMBL:AA007328
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                                                                                   dbSTS:STS18321
                                                                                                                   Identified using the e-PCR software 128419. .128543
                                                                                                                                        dbsts:sts25817
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         Identified using the e-PCR software (G. 138509. .138658
                             dbsrs:srs42930
                                          RHdb: RH53972
                                                               138462. .138738
                                                                                                 RHdb:RH53698
                                                                                                                                                              /note="matching EMBL: H22648
/note="matching EMBL:M78864
                                                                       Identified using the e-PCR software
                                                                                                        /note="matching EMBL:R87257
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89946 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                                                                   301 gtctttggggctgccctgtgtgcctgagagtgtccaacaaagaaatggagcctttggtggga 360
                                                                                                                                                                                                                                                         181 ttetetgaeettggeegeteagetacaegtgaeeceaggeteageeeageaaegetteaee 240
                                                                                                                                                                                                                                                                                                                                                                                   TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC
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            agtggcggctggg 433
                                                                     caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
AGTGGGGGCTGGG
                                                          GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
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Identified using the e-PCR software
161617. .161761
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Identified using the e-PCR software 138805. .138926
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138568. .138647
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RHdb:RH68657
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RHdb:RH76320
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Identified using the e-PCR software
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RHdb:RH92419
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91.2%;
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Listing first 45 summaries
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                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
             TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                            REGISTRATION NUMBER: 32,893
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                     herewith
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                                             1483.0140002
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; STRANDEDNESS:
; TOPOLOGY: botl
; MOLECULE TYPE: c
US-08-978-523-2
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US-08-798-897-1
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                                                                                                                                                                                             Sequence 1, Application US/08798897 Patent No. 5789201
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Guastella,
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  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                          NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                      TITLE OF INVENTION:
                           STATE: DC
COUNTRY: US
ZIP: 20005
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LENGTH: 579 base pairs
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                                                                                1100 New York Avenue, N.W., Suite
                                         USA
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99.3%;
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Pred. No. 1.8e-140;
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Thu Jun

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US-08-978-523-1
sequence 1, Application US/08978523
patent No. 5883229
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301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
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APPLICANT: Guastella, John
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,89
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
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LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
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                                                                                                                                      121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCCGCTTCCGGCGCACC 180
                                                                                                                                                                                                                                                                                                 121 ccgctgcaccaagccatgcgggcagcttggagatgagttcgagacccgcttccggcgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                     301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
361 CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC
                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 90.5%; Score 527.8; DB 2;
Local Similarity 94.5%; Pred. No. 8.5e-129;
                                                                                                                                                                                                                                                                                                                                                                                                                       1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                                                         ttetetgatetggeggeteagetgeatgtgaceceaggeteageceageaacgetteaec 240
                                                                     GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCATTGGTGGGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547;
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1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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; MOLECULE TYPE: US-08-798-897-1

INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 579 base pairs

LENGTH:

TYPE: nucleic acid STRANDEDNESS: both

TOPOLOGY: both

CDNA

TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600

TELEFAX:

202-371-2540

REGISTRATION NUMBER: 32,893 REFERENCE/DOCKET NUMBER: 14

1483.0140001

NAME: Esmond, Robert W. REGISTRATION NUMBER: 32

ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

CURRENT APPLICATION DATA:

SOFTWARE: COMPUTER: IBM PU OPERATING SYSTEM:

PatentIn Release #1.0, Version #1.30

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

APPLICATION NUMBER: FILING DATE: Februa

February 11, 1997

US/08/798,897

Matches Query Match

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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312-755-4489 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPACTION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
218 gctcagcccagcaacgcttcacccaggtctccgacgaactttttcaagggggccccaact 277
                                 424 TTGAACTGCGGTACCGGCGGCATTCAGTGACCTGACATCCCAGGCTCCACATCACCCCAG 483
                                                              158 togagacocgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thompson, Craig B.
APPLICANT: Boise, Lawrence H.
TITLE OF INVENTION: Vertebrate Apoptosis Gene
TITLE OF INVENTION: Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Chicago
                                                                                                                               98 cc9999ag99cccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: NO. 5646008thrup, Thomas E. REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 ggggccctggtaactgtaggggccttttttgctagcaag 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           481
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                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312-744-0090
TELEFAX: 312-755-4489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 60610
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                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                          Conservative
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135..836
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                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/081,448
                                                                                                                                                                       0; Mismatches 190; Indels
                                                                                                                                                                                      Score 131; DB 1; Length 926; Pred. No. 2.2e-25;
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; LOCATION: US-08-470-670A-6
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Patent No. 5834309 5710045
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                                                                                                                                                                                                                                                                                                                   TELEFAX: (512) 474-7577 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Thomps
APPLICANT: Boise,
                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING MALE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: VERTEBRATE APOPTOSIS GEN
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                                                                                                                                        TOPOLOGY:
                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603
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                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houston
                                                                                                                                                                                                                                           926 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Arnold, Wh
P.O. Box 4433
                                                                CDS
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                              135..836
                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIV.
TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 TTGAACTGCGGTACCGGGGCATTCAGTGACCTGACATCCCAGCTCCACATCACCCCAG 483
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                                                                                                                                          APPLICATION NUMBER: US 08/435,518 FILING DATE: 04-MAY-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGTGGAACTCTATGGGA 723
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Local Similarity 56.3%;
hes 245; Conservative
                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            724 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783
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                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 tgctgacgggggccg 532
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
STATE:
                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Poloco
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                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                            REFERENCE/DOCKET NUMBER: RPI-034CP
                                                                                                          NAME: DeConti, Giulio A. (GAD)
REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGTCGCATTGTGGCCTTTTTCTCCTTCGGCGGGCACTGTGCGTGGAAAGCGTAGACA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggggccgccttgtagccttctttgtctttggggctgcactgtgtgctgagagtgtcaaca 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCCGGGATGGGGTAAACT 543
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                                                                                                                                                                                                                                                                                                                                                                               02109
                                                                                                                                                                                                                                                                                                                                                                                                                                     Boston
                                                                                                                                                                                                                                                                                                                                                                                                                 Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June, Carl H. and Thompson, Craig B. VENTION: METHODS FOR ENHANCING T CELL
                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAHIVE & COCKFIELD
                                                                                                                                                                                                                                07-JUNE-1995
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Best Local Similarity 56.3%;
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                                                                                                                                                   SEQ ID NO
                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/167,921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                       APPLICANT: Nickoloff, Brian J.

APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
FILE REFERENCE: ISPH-0324
                                                                                                                                                                                                                                                                                                                  APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
NAME/KEY: CDS
LOCATION: (135)..(836)
PUBLICATION IMFORMATION:
DATABASE ACCESSION NUMBER: L20121 Genbank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                           ORGANISM: Homo sapiens
                                                                         FEATURE:
                                                                                                             TYPE: DNA
                                                                                                                                 LENGTH:
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Pred. No. 2.2e-25;
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US-09-167-921-1

DATABASE ENTRY DATE: 1994-07-26

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CURRENT APPLICATION NUMBER: US/09/277,020
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 39
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
US-09-277-020-39
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                                                                                                                                   Matches 245;
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/09277020 Patent No. 6210892
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation TITLE OF INVENTION: of mRNA Processing FILE REFERENCE: ISPH-0339
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bennett, C. Frank
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158 togagacocgcttccggcgcaccttctctgatctggcggctcagctgcatgtgaccccag 217
                                                 98 ccggggagggcccagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
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                                                                                                                                       22.5%; Score 131; DB 4; Length 926; 56.3%; Pred. No. 2.2e-25;
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CURRENT APPLICATION NUMBER: US/09/323,743
CURRENT FILING DATE: 1999-06-01
EARLIER APPLICATION NUMBER: 09/277,020
EARLIER FILING DATE: 1998-03-26
EARLIER FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 09/167,921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 926
                                                                                                                                                                                                                                                                                                                                             ; LUCATION: (135)...(836)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-323-743-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09323743 Patent No. 6214986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett p.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
218 gctcagcccagcaacgcttcacccaggtctccgacgaactttttcaagggggccccaact 277
                                            424 ttgaactgcggtaccggcgggcattcagtgacctgacatcccagctccaccatcaccccag 483
                                                                      158 tcgagacccgcttccggcgcaccttctctgatctggcggctcagctgcatgtgacccag 217
                                                                                                                                 98 ccggggagggcccagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
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                                                                                                                                                                                                                                     245; Conservative
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                                                                               NAME/KEY: CDS
LOCATION: 135..836
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-461-511A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08461511A Patent No. 6303331 GENERAL INFORMATION:
Best Local Similarity 56.3 Matches 245; Conservative
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               484 ggacagcatatcagagctttgaacaggtagtgaatgaactcttccgggatggggtaaact 543
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INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,511A
APPLICATION NUMBER: US/08/461,511A
FILING DATE: 05-Jun-1995
CLASSIFICATION: UNKNOWN
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:179
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctggagacgc 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Thompson, Craig B.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Houston
                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                   LENGTH: 926 base pairs
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                      22.5%; Score 131; DB 4; 56.3%; Pred. No. 2.2e-25;
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         Mismatches 190;
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                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPAT
OPERATING SYSTEM: PC-DO:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT.
FILING DATE: CONCURRENT
                                                                                            TELEPHONE: 512-320-720
TELEFAX: 713-789-2679
INFORMATION FOR SEQ.ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 ggctggctgactggatccacagcagtggggggctgggagttcacagctctatacgggg 457
                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/01 FILING DATE: 22 JUNE 199: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                    NAME: PARKER, David L. REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                               CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cogggaagggcocagcagctgacccgctgcaccaagccatgcgggcagctggagatgagt 157
                                         TYPE: nucleic acid
STRANDEDNESS: sing
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                              TOPOLOGY: linear
                                                                             LENGTH:
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                                                                                   926 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS, ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                  UMBER: PCT/US94/07089
CONCURRENTLY FILED
                                                                                                                                                                                                                                                                22 JUNE 1993
                                                 single
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US-08-465-485A-20
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                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
                                             FILING DATE: 05-JUN-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA
                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                 APPLICATION NUMBER: US 0 FILING DATE: 20-SEP-1993
                                                                                                                                                                                                                                                                            STREET: 1755 S.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784 GCATGACTGTGGCCG 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                                                                                                                                                                          1755 S. Jefferson Davis Hwy., Suite 400
                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Reed, John
                                                                                                                                                                                                                                                                                                                             OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
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                                US 08/124,256
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US-09-080-285-20
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                                                                                                                                                                                  Sequence 20, Application US/09080285 Patent No. 6040181
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US-08-465-485A-20
                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                         APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
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INFORMATION FOR SEQ ID NO:
        STREET: 1755 S. Jefferson Davis Hwy., Suite 400 CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                   604 TACGG 608
                                                                                                                                                                                                                                                                                                                   451 tacgg 455
                                                                                                                                                                                                                                                                                                                                       544 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG 603
                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                         484 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG
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LENGTH: 717 base pairs
TYPE: nucleic acid
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FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-SEP-1993
PRIOR APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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LENGTH: 717 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                         244 GCGGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGGC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08 FILING DATE: 05-JUN-1995
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                                                                544 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAACTG
                                                                                                                                                       331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg
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604 TACGG 608
                                451 tacgg 455
                                                                                                                                   484 GTCAACCGGGAGATGTCGCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG
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                                                                                                                                                                                                                                                                      ACGCCCTTCACCGCGCGGGGACGCTTTGCCACGGTGGTGGAGGAGCTCTTCAGGGACGGG 423
                                                                                        gagacgcggctggctgactggatccacagcagtgggggctgggcggagttcacagctcta 450
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Search completed: June Job time: 4718 sec

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tsujimoto, Yoshide; Croce, Carlo A. TITLE OF INVENTION: DNA MOLECULES HAVING HUMAN BCL-2 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 18-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                1942 gtcaaccgggagatgtcgcccctggtggacaacatcgccctgtggatgactgagtacctg 200:
                                                                                                                                                                                                                          1822 acgcccttcaccgcgcggggacgctttgccacggtggtggaggagctcttcagggacggg 1881
                                                                                                                                                                                                                                                                                                                                                                               1702 gcggggcctgcgctcagcccggtgccacctgtggtccacctggccctccgccaagccggc 1761
                                                                      2002 aaccggcacctgcacacctggatccaggataacggaggctgggatgcctttgtggaactg 2061
2062 tacgg 2066
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                                                                                                                                                                      331 gtcaacaaggagatggaaccactggtgggacaagtgcaggagtggatggtggcctacctg 390
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                                                                                              391 gagacgcggctggctggattggattccacagcagttgggggctgggcggagttcacagctcta 450
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FILING DATE: 23-DEC-1992
APPLICATION NUMBER: 653,010
FILING DATE: 19-MAR-1991
APPLICATION NUMBER: 883,687
                                      451 tacgg 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 21.2%;
Local Similarity 58.6%;
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pred. No. 3.4e-23;
0; Mismatches 151;
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
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                                                                                                                                                                                   Result
No.
 pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                         554.8
553.2
527.6
527.6
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488.2
422.4
422.4
400.2
380.2
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369
362
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241.6
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583
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Listing first 45 summaries
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AK015644
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BF204905
BG677345
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    AL157542 DKFZP761D
BE793530 601590016
AK015644 Mus muscu
BE793580 Mus muscu
BE770566 603060362
BI910270 603069493
BF785386 602111728
AK013244 Mus muscu
BC298789 602396527
AW258810 um74a02.y
BT764428 603050701
BF204905 601866718
BG677345 602624059
AA556919 v021f08.r
AW356901 20104 MAR
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ALIGNMENTS

150 a	BASE COUNT
/organism "Homo Saphens /db_xref="taxon:9606" /clone="DKFZP761D0816" /clone_1bb="761 (synonym: hamy2)" /tissue_type="amygdala" /dev_stage="adult"	
	FEATURES source
German Genome Project.  No s1 sequence available.  No s1 sequence available is available at the RZPD in Berlin.  This clone (DKFZp761D0816) is available at the RZPD in Berlin.  Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  Perlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.	
Am Klopferspitz 18a D-82152 Martinsried, Germany Am Klopferspitz 18a D-82152 Martinsried, Germany Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert This is the 5' sequence of the clone Analysis, German Cancer Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. wiemannedkfz- heidelberg.de; Research Center (DKFZ); Email s. wiemannedkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories,	·
1 (bases 1 to 804) Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.) EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.) Unpublished (1999) Contact: Ansorge W	REFERENCE AUTHORS TITLE JOURNAL COMMENT
EST. human. Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini;	KEYWORDS SOURCE ORGANISM
AL157542.1 GI:7057943	ACCESSION
AL157542 BO4 bp mRNA linear EST 24-FEB-2000 DKF250761D0816_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKF27761D0816_r, mRNA sequence.	RESULT 1 AL157542 LOCUS DEFINITION

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 cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 1030) NIH-MGC http://mgc.nci.nih.gov/.
Plate: LLCM800 row: p column: 04
                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                    National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                              Eukaryota;
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                                                                                                                                                                                                                                                                                                                                601590016F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944307
                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                          BE793530.1 GI:10214832
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Pred. No. 6.3e-116;
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DEFINITION AK015644 RESULT

AK015644 1949 bp mRNA linear HTC 19-3 Mus musculus adult male testis cDNA, RIKEN full-length enrical library, clone:4930488D08:Bc12-like 2, full insert sequence

RNA linear HTC 19-JAN-2002 RIKEN full-length enriched

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                  541 9999ccctggtaactgtagggggcctttttttgctagcaagtga 582
684 GGGGCCTGGGTAACTGTAGGGGCCTTTTTGCTAGCAAGTGA 725
                                                                                    481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
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                                                              caggtotocgaegaetttttcaagggggcoccaactggggcogcottgtagcottottt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="organ: lung; vector: pOTB7; Site_1: XhOI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500p for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Stratagene) and Superscript II RT (Life Technologies)."
284 c 386 g 170 t
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/cell_line="MGC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:3944307"
/clone_lib="NIH_MGC_7"
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Pred. No. 1.6e-115;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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5 (bases 1 to 1949)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-UII-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-UII-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha RIKEN Yokohama Institute; 1-7-25 Suehiro-cho, Tsurumi-ku, Yokoha RIKEN Yokohama Institute; 1-7-25 Suehiro-cho, Tsurumi-ku, Yokohama Institute; 1-7-25 Suehiro-cho, Tsurumi-ku,
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Hayashizaki,Y.
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552 AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCCTGGAGGAGGCACGG 611
                                  421 agtgggggctgggggggttcacagctctatacggggacgggggccctggaggaggcgcggg 480
                                                                                                                                             492 CAAGTGCAGGATTGGATGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC
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/db_xref="G1:12894053"
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                                        Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, M., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hara, A., Hayatsu, M., Hiraoka, T., Hori, F., Harai, A., Hayatsu, M., Hiraoka, T., Hori, F., Harai, A., Hayatsu, M., Hiraoka, T., Hori, F., Harai, A., Hayatsu, M., Hayatsu, M., Hiraoka, T., Hori, F., Harai, A., Hayatsu, M., Hay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yojiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequences cenome Res. 10 (11), 1757-1771 (2000)
Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                                                                                                                               Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
                                                                                                                                                                                             Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

5. (bases 1 to 3487)
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High-efficiency full-length cDNA cloning
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241 caggtctccgacgaactttttcaagggggccccaactggggccgccttgtagccttcttt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome
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/db_xref="GI:12836028"
/translation="MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
AMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
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/note="Bcl2-like 2
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209. .790
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603060362F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5209862 5',
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: LLAM11526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                      /note-"organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1,4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note:
                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5209862"
/clone_lib="NIH_MGC_122"
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                                                                                                                                                                                                           AUTHORS
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   Email: cgapbs-r@mail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11548 row: j column: 23
High quality sequence stop: 643.
                                                                                                                                                                                                                                                                                                                                                                 603069493F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218294 5',
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                             NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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98.6%;
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Pred. No. 7.9e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 caggteteegaegaaettttteaagggggeeceaaetggggeegeettgtageettettt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCCAGGCTCAGCCCAACAACGCTTCACC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                       Mus musculus
                                                                                                                                                                                                                              602111728F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798
                                                                                                                                                                               BF785386.1 GI:12090422
                                                                                                                                                                                                         BF785386
                                                                                                                                                                                                                                                               BF785386
                                                                                                                                            house mouse
                                                           mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; (bases 1 to 815)
                                                                                                                                                                                                                    mRNA sequence.
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/clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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94.3%;
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                                   561 ggccttttt 569
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                                                                                   501 ggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctgggtaactgtagg
                                                                                                                                       416 CACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG-GTCTGCGGGAGGGGAAC-G
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GCCTTTTT 541
                                                               GGCATCAGTGAGGACAGTGCTGACGGGGGCCGTGGCACT-GGGGCCCTGGTAACTGTAGG
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                                                                                                                                                                                                                                                                                           TGCTGAGAGTGTCAACAAAGAAATGGAGCC-TTGGTGGGACAAGTGCAGGATTGGATGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM9853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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/Clone_lib="NCI_CGAP_Kid14"
/Lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/Site_2: Sall; Cloned unidizectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 212 c 296 g 141 t
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/db_xref="taxon:10090"
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                                                                                             Submitted (10-JUL-2000) voshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN YOKohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax.81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5 (bases 1 to 854)
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                                                               please visit our web site (http://genome.gsc.riken.go.jp/) for
cDNA library was prepared and sequenced in Mouse Genome
                                 further details.
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                          121 ccgctgcaccaagccatgcgggcagcttggagattgagttcgagacccgcttccggcgcacc 180
                                                                       496 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 555
                                                                                         301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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                                                                                                                                                                                 241 caggiotocogacgaactttttoaagggggccccaactggggccqccttgtagccttottt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
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                                                                                                                                                                                                                                                                                                      CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
CAAGTGCAGGATTGGATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to
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196. .732
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/protein_id="BAB28740.1"
/db_xref="GI:12850488"
/dtanslation="MATPASTPDTRALVADFYGYKLROKGYVCGAGPGEGPAADPLHQ
/translation="MATPASTPDTRALVADFYGYKLROKGYVCGAGPGEGPAWGRLYAFFVF
AMRAAGDEFETRERETESDLAAQLHVTPGSAQQRETQVSDELFQGGPWWGRLYAFFVF
GAALCAESVNKEMEPLYGQVQDWMVAYLETRLADWIHSSGGWVRSSQLLLLSASLYKVG
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/note="BCl2-like 2
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                                         301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
                                                                                                                      279 TTCTCTGACCTGGC-GCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACC 337
                                                                                                                                             181 ttetetgatetggeggeteagetgeatgtgacceeaggeteageceaggeteaece 240
                                                                                                                                                                                                                           121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                                                                                                                                               159 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGGCCCTGGGGAAGGCCCCAGCCGCCGAC 218
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                                                                                                                                                                                                    CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC
                                                                                                                                                                                                                                                                                                                                                          ATGGCGACCCCAGCCTCAACCCCCAGACACACGGGCTCTAGTGGCCTGACTTTGTAGGCTAT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10394 row: e column: 08
High quality sequence stop: 713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="retina"
//ab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:4511215"
/clone_lib="NIH_MGC_94"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:1009678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
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IMAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                     /clone_lib="Sugano mouse kidney mkia"
/sex="female"
                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:2300906"
                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL"
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Best Local Similarity

62.1**%**; 91.6**%**;

Score 362; DB 9; Pred. No. 3.2e-72;

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11477 row: a column: 01
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Tissue Procurement: Life Technologies, Inc.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
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                          /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); source anonymous pool of 3 colons, age 26 yo male, 49
                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5190792"
                                                                                                    /clone_lib="NIH_MGC_116"
                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                      ocation/Qualifiers
71 yo male colon; 46 yo male kidney, and pool of 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601866718F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106836 5',
                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF204905.1 GI:11098491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                              Plate: LLCM987 row: d column: 05 High quality sequence stop: 561.
                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM987 row: d column: 05
                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                      cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can
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/clone="IMAGE:4106836"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                ocation/Qualifiers
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98.2%;
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Pred. No. 1.5e-64;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             602624059F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4748943 5',
                                                                                                                                                                                                                                                                                                                                                               BG677345.1 GI:13908742
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/note="Organ: muscle; Vector: pOTB7; Site_1: ECORI;
Site_2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 176 c 201 g 114 t
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Pred. No. 6e-57
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Local Similarity 99.0%;
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                                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                               The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                              Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA596919 362 bp mRNA linear EST 19-SEP-19: VO21f08.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1050567 5' similar to TR:E123735 E123735 Rl MRNA. ;, mRNA
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA596919.1 GI:2412354
                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://image.llnl.gov
Plate: LLAM10601 row: f column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                        (bases 1 to 362)
                          314 286 1800
314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="squamous cell carcinoma"
/tlab_host="DH10B (T1 phage-resistant)"
/note="0rgan: skin; vector: pcWv-SpPRT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 239 c 219 g 135 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:4748943"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Skn4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 294.2; DB 1
Pred. No. 8.7e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 19-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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FEATURES
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                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                 AW326901
                                             REFERENCE
                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                          ORGANISM
                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 ctgcaccaagccatgcgggcagcttggagattagagttcgagacccgcttccggcgcaccttc 183
                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                      304 tttggggctgcactgtgtgctgagagtgtcaacaag 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 gtctccgacgaactttttcaagggggccccaactggggccgccttgtagccttctttgtc 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 ctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgacccg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 gogaccocagcctcggccccagacacacgggctctggtggcagactttgtaggttataag 63
                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCACCAAGCCATGCGTGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCCGCACCTTC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTGAACTGGCCGCTCAGCTACACGTGACCCCAGGCTCAGCCCAGCAACGCTTCACCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                GTTTCCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCCGTCTTGTGGCATTCTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              totgatotggoggotoagotgcatgtgaccccaggotoagoccagcaacgottcacccag 243
                                                                                                                                                                                                                                                                                                                                                   TTTGGGGCTGCCCTGTGTGCTGAGAGTGTCACAAAG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: -28m13 rev2 ET from Amersham
                                                                                                                                                              AW326901.1 GI:6762822
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
1 (bases 1 to 433)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Smith, T.P.L., White, J., Cho, J., Fahrenkrug, S.C., Bennett
                                                                                   Bos taurus
Bos taurus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea
                                                                                                                                                                                                                             20104 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                               COW
                                                                                                                                                                                                                                                  AW326901
                                                                  Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: p77T3D-Pac (Pharmacia) with a modified /note="Vector: p7TT3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' regrace of the modified primer stranded by Bob Barstead. The C2C12 cell line cavailable from ATCC. catalog # CRL-1772) differentiates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rapidly, forming contractile myotubes and producing characteristic muscle proteins. " 116 c 107 g 75 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1050567"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C3H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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91.4%;
                                                                    Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                        433 bp
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                                                                                                                                                                                                                                                        mRNA
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                                                                                                Pecora; Bovoidea;
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Search completed: June Job time: 5585 sec

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2002, 11:24:29

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                        154 ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTAGTGGCAGACTTTGTGGGCTAT 213
                                                                                                                                                    274
                                                                                                                                                                                                                                 214
                  241 caggtctccgacgaactttttcaagggggccccaactggg 280
                                                                             334
                                                                                                                 181
                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                           1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                  CCGCTACACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 333
                                                                                                                                                                                                                               AAGCTGAGGCAGAAGGGGTATGTTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC
CAGGTCTCTGATGAACTCTTCCAAGGGGGCCCCAACTGGG 433
                                                                         ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                     ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc 240
                                                                                                                                                                                                                                                                                                                                                                                        266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 11 (4), 626-630 (2001)
21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG
Plate: 10 row: G column: 24
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single pass sequencing. Bases called and trimmed with phred v0.980904.e. vector identified by cross_match with the -mins and _minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          44.2%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 257.6; DB 9;
Pred. No. 1.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 g
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 433;
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Thu Jun

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Title:
Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
Result
No.
                                                                      pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 6, 2002, 09:53:19 ; Search time 1853.13 Seconds (without alignments) 6583.548 Million cell updates/sec
Query
Match Length DB
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1797656 segs, 10463268293 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atggcgaccccagcctcggc.....cttttttgctagcaagtgaa 583
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Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_om:*
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## ALIGNMENTS

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                                                        TITLE
                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 582)
Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.
bcl-w, a novel member of the bcl-2 family, promotes cell survival
Oncogene 13 (4), 665-675 (1996)
Cory,S.
Direct Submission
Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and
Submitted (03-JUN-1996) Medical Research, PO Royal Melbourne
                                                                                                                                                                                                                                                                                                                                                                                         Human Bcl-w (bcl-w) mRNA, complete cds. U59747
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                                                                                             2 (bases 1 to 582) Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M.
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                                                                                                     GGGGCCCTGGTAACTGTAGGGGCCTTTTTTGCTAGCAAGTGA 582
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Human mRNA for KIAA0271 gene,
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/Protein_10" ABD9055.1"
/Gb_xref="GI:1572493"
/Ctranslation="MATPASAPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQ
/Ctranslation="MATPASAPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQ
AMRAAGDEFETAFRTRETSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQEWMVATLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                        ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgattcacc
                                                                                                                                                              ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                       TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAGGCTCAGCCCAACAACGCTTCACC
                                                                                                                                           CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC
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                                                                                                                                                                                                                                                                                                                                                             581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
Direct Submission
Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Rese
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
1. 3542
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Nagase,T., Seki.N., Ishikawa,K., Ohira,M., Kawarabyasi,Y., Ohara,O., Tanaka,A., Kotani.H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human genes. V The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced analysis of cDNA Clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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amraagdefetrfrrtfsdlaaglhvtpgsagorftovsdelfoggpnwgrlvaffvf
gaalcaesvnkemeplygovoewmvayletrladwihssggwaeftalygdgaleear
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177. .758
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/clone_lib="pSPORT 1
177. .758
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/db_xref="GI:1944418"
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/db_xref="taxon:9606"
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99.7%;
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Pred. No. 1.1e-118;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGCCCTGGTAACTGTAGGGGCCCTTTTTTGCTAGCAAGTGAA 759
                                                                                                                                                                                               atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC 180
                                                                                                                                                                                ATGGCGACCCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
                          ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagcaacgcttcacc
                                                                          ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                     AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCAGCAGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes Patent: EP 0932674-A 6 04-AUG-1999; AMRAD OPERATIONS PTY LTD (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
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RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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AMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPWGRLYAFFLF
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121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc
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                                               aagctgaggcagaagggttatgtctgtggagctggcccgggggagggcccagcagctgac 120
                                                                                            ATGGCGACCCCAGCCTCGGCCCCAGACACGCGCTCTGGTGGCAGACTTTGTAGGTTAT 60
                               AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, J.M., Holmgreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bcl-w, belongs to the bcl-2 family of apoptosis-controlling genes patent: WO 9735971-A 6 02-CCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified
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                                                                                                                                                             Conservative
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a 157 c 210 g 111 t
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Clone distribution: MGC clone distribution information can be fo
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 15 Row: k Column: 19
                                                                                           Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                         DNA Sequencing by: Nations Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                          CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                Web site:
                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                         http://www.nisc.nih.gov/
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2, clone MGC:10675
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IMAGE:3944307, mRNA,
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//db_xref="G1:18203707"
/db_xref="G1:18203707"
/translation="MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQ
AMRAAGDEFETTAFRTFSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRIVAFFVF
GAALCAESVINKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGGWASVRTUTGAVALGALVTVGAFFASK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Lung, small
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
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/db_xref="LocusID:599"
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1. .1437
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Pred. No. 2.6e-118;
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Patent: US 5789201-A 2 04-AUG-1998;
Location/Qualifiers
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        Rattus norvegicus
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                   Norway rat.
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99.3%;
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Pred. No. 5e-117;
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                                                                                             gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCCTGGAGGAGGCACGG
                                                                               CAAGTGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC
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Submitted (01-007-1998) Developmental Neuroscience, Uppsala
University, Box 587, BMC, Uppsala 751 23, Sweden
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/protein_id="AAC64200.1"
/protein_id="AAC64200.1"
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/translation="MATPASTPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQ
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GAALCAESYNKEMEDLVGQVQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLTGAVALGALVTVGAFFASK"
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/db_xref="taxon:10116"
/tissue_type="brain"
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9999ccct99taact9tag9g9gcctttttttgctagcaag
                                                                                                     agtgggggctgggcggagttcacagctctatacggggacgggggccctggaggaggcgcgg
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                                                                                      AGTGGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCCTGGAGGAGGCACGG
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                                                                                                                                                                                                       AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCCAGCCGCCGAC
                                                                                                                                                                                                                                                                                                                                                    548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-JUN-1996) Molecular Biology Unit, The Walter an Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            582 bp
Mus musculus Bcl-w (bcl-w) mRNA,
U59746
U59746.1 GI:1572494
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/Protein_id="AB09056.1"

/db_xref="GI:1572495"

/translation="Mattrastpottralvadevgyklrokgyvcgagpgegpaadplho
/translation="Mattrastpottralvadevgyklrokgyvcgagpgegpaadplho
AMRAAGDEFETRERRIFSDLAAQLHVIPGSAQQRETQVSDELFQGGPNWGRLVAFFVF
GAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEAR
RLREGNWASVRTVLIGAVALGALVTVGAFFASK"

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/db_xref="taxon:10090"
/chromosome="14"
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ss,A.J. and MacGregor,G.R.
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                        Adams, J.M., Holngreen, S.P., Cory, S. and Gibson, L.M. Adams, J.M., Holngreen, S.P., Cory, S. and Gibson, L.M. A novel mammalian gene, bol-w, belongs to the bcl-2 apoptosis-controlling genes patent: EP 0932674-A 8 04-AUG-1999; AMRAD OPERATIONS PTY LTD (AU)
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Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
A novel mammalian gene, bcl.w, belongs to the bcl-2 family of
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GAALCAESVNKEMEPLVGQVODWIVAYLETRLADWIHSSGGWADFTALYGDGALEDAR
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/db_xref="taxon:32644"
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Pred. No. 3.2e-102;
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                      from chromosome 14 of Homo sapiens (Human), complete sequence
                                          LNSUUUUB 196292 bp DNA linear PRI 22-MAY-Human chromosome 14 DNA sequence BAC R-124D2 of library RPCI-11
AL049829.4 GI:8217859
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Patent: WO 9735971-A 8 02-OCT-1997;
ADAMS JERRY MCKEE (AU); HOLMGREEN SHAUN P (AU); CORY SUZANNE (AU); GIBSON LEONIE M (AU); AMRAD OPERATIONS PTY LTD (AU)
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/db_xref="taxon:32644"
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Pred. No. 3.2e-102;
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STS	STS	STS	FEATURES SOUICE				COMMENT	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	REFERENCE	KEYWORDS SOURCE ORGANISM
RHdb:RH/8//3 dbSTS:STSS514 IdentLified using the e-PCR software (G. Schuler) IdentLified using the e-PCR software (G. Schuler)  9358093808 /note="matching EMBL:AA007328 RHdb:RH75103	"match H98727 STS684 fied u .8229	/clone="R-124D2" /clone_lib="RPCI-11" /clone_lib="RPCI-11" /R25978398 /R859978398 /note="matching EMBL:AA908790 RHdb:RH102162 dbs78:S7869699 Identified using the e-PCR software (G. Schuler)" RN43380566	90 - 99 :	20 - 29 : 10 30 - 39 : 30 40 - 49 : 829 50 - 59 : 1909 60 - 69 : 5193 70 - 79 : 18093	rall qual		On Jun 3, 2000 this sequence version replaced g1:6138746. On Jun 3, 2000 this sequence version replaced g1:6138746. Center: Genome Center Center: Genoscope / Centre National de Sequencage Center code: GS Center tode: GS Ce	Nat	Eukaryota: Metazoa: Chordata: Craniata; Verlebiata; Fuccessian de la composition del composition de la composition de la composition de la composition del composition de la c	) 
Db 89826 ATGG Qy 61 aagct       Db 89886 AAGC	Query Ma Best Loc Matches	BASE COUNT 5	STS	STS	STS STS	STS	STS	STS	STS	STS
AllGalanchechaech (1980) AllGalanchechaech (19	tch 73.4%; Score 428.2; DB 9; Length 100.2; al Similarity 99.3%; Pred. No. 3.1e-85; al Similarity 99.3%; Indels 0; Gaps 0; al Similarity 99.3%; Indels 0; a	107 107 197 the e-PCR softwar 17123 g 52626 t	g g	Inote "matching EMBL.H72023  RHdb:R128671  dbsTs:STS20163 Identified using the e-PCR software (G. Schuler)"  138805138926 Inote "matching EMBL:H72023  RHdb:RH68657	EMBL:	RHdb:RH53972 dbSTS:STS42930 Identified using the e-PCR software (G. Schuler)	RHdb:RH53698 dbSTS:STS18321 Identified using the e-PCR software (G. Schuler)" 138462138738 /note="matching EMBL:R59134	EMBL: H22648  the e-PCR software (G. SEMBL: R87257)	e-PCR :D11677	dbSTS:STS52191 Identified using the e-PCR software (G. Schuler)" 107758107951 /note="matching EMBL:R94929

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-SEP-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On NOV 8, 2000 this Sequence version replaced gi:10179358.
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Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Gupta,J.,
Ho,S.-L., Idol,J., Karlins,E., Lee-Lin,S.-Q., Legaspi,R., Lim,M.,
Maduro,Q.L., Maduro,V.B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Prasad,A., Snyder,B., Stantripop,S.,
Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D. and Green,E.D.
NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 147800 bases at least Q40 consensus quality: 148726 bases at least Q30 consensus quality: 14933 bases at least Q20 Insert size: 145000; agarose-fp Insert size: 150812; sum-of-contigs Quality coverage: 11.76x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                          Center project name: 24
                                                                                                                                                                                                                                                                                                        Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                           Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                Center: NIH Intramural Sequencing Center Center code: NISC
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74875 CAAGTGCAGGATTGGATGGTGGCCTACCCAGAGACACGCCTGGCTGACTGGATCCACAAC 74934
                                                                                       74815 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAGAAAATAGAGCCATTGGTGGGA 74874
                                                                                                                                                                             74755 CAGGTTTCCAACGAACTTTTCCAAGGGGGCCCCAACTAGGGCCATCTTGTGACATTCTTT 7481
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                       301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
                                                                                                                                                                                                            241 caggtctccgacgactttttcaagggggccccaactgggggccgccttgtagccttcttt 300
                                                                                                                                                                                                                                                                                            181 ttetetgatetggeggeteagetgeatgtgaceceaggeteageeeaggeaacgetteaee 240
                                                                                                                                                                                                                                                                                                                                                                                    121 ccyctycaccaagccatycygygcayctygayatyayttcgayaacccycttccgycgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
110466. .151212
/note="assembly_fragment"
.30838 c 31177 g 45417
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65653. .110365
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/clone_lib="RP31"
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/chromosome="4"
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/strain="Brown Norway"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%; Score 388.6; DB 2
83.9%; Pred. No. 1.9e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Dietrich, N.L., Gupta, J., Ho, S.-L., Idol, J., Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, O.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Snyder, B., Stantripop, S., Thomas, J.W., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tran, J.T., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D. NISC Mouse Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus chromosome 4 clone RP31-103L21 st
Norway, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
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                                            * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-OCT-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jnpublished
                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: phrap; version 0.990319
Assembly program: phrap; version 0.990319
Consensus quality: 179798 bases at least 040
Consensus quality: 180132 bases at least 030
Consensus quality: 1801274 bases at least 020
Consensus quality: 180274 bases at least 020
Insert size: 180000; pulse-field-gel
Insert size: 180000; pulse-field-gel
Insert size: 180982; sum-of-contigs
Quality coverage: 15.02x in 020 bases; pulse-field-gel
Quality coverage: 112.95x in 020 bases; sum-of-contigi
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Center clone name: 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----- Summary Statistics
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5430: contig of 5430 bp in length 5530: gap of unknown length
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4 clone RP31-103L21 strain Brown
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                                                                                                                                                                                                                                                                                                                                                 pulse-field-gel
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FEATURES
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Best Local Similarity 83.9%;
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                                                                                                                                                                                                                                                                            50039 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAGAAAAATAGAGCCATTGGTGGGA 50098
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                                                                  misc_feature
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50159 ANTGGGGGCTGGGTGGAGTTCACAGCTCTATTCCGGAATGGGGCCCTAGAAGAGACATGG
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                                                                                                                                                          421 agtgggggctgggcggagttcacagctctatacggggacgggggccctggaggaggcgcgg 480
                                                                                                                                                                                                        301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga 360
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ture 85893. .181282
/note="assembly_fragment"
50811 a 36290 c 37296 g 56560 t
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39604. .85792
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/chromosome="4"
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39603: gap of unknown length
85792: contig of 46189 bp in length
85892: gap of unknown length
181282: contig of 95390 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .39503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 388.6; DB 2
Pred. No. 1.9e-76;
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Search completed: June 6, Job time: 7495 sec

2002, 11:58:14

OM nucleic - nucleic search, using sw model GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Title: Perfect score: Sequence: June 6, 2002, 10:44:02; Search time 295.22 Seconds (without alignments) 3390.580 Million cell updates/sec US-09-155-327E-6 583 1 atggcgaccccagcctcggc.....cttttttgctagcaagtgaa 583

Run on:

Scoring table: Gapop 10.0 , Gapext 1.0 IDENTITY\_NUC

1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Listing first 45 summaries Match 100%

Database :

N\_Geneseq\_032802:\*
1: /SIDS1/gcgdata/gc2: /SIDS1/gcgdata/gc3: /SIDS1/gcgdata/gc3: /SIDS1/gcgdata/gc4: /SIDS1/gcgdata/gc5: /SIDS1/gcgdata/gc5: /SIDS1/gcgdata/gc6: /SIDS1/gcgdata/gc6: /SIDS1/gcgdata/gc9: /SIDS1/gcgdata/gc9: /SIDS1/gcgdata/gc9: /SIDS1/gcgdata/gc9: /SIDS1/gcgdata/lc2: /SIDS1/gcgdata/lc2: /SIDS1/gcgdata/lc2: /SIDS1/gcgdata/lc3: /SID N. Geneseq. 032802:\*

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SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*

SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:\*

RESULT 1 AAT96577

AAT96577 standard; DNA; 583 BP.

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length DB	ength		ID	Description
	1 1 1 1 1		1 1 1 1			Times bol -w DNA
٠.	578.2	99.2	583	18	AAT96577	Human Det w Diva
ا د	579 )	99 2	583	20	AAX25134	Human bcr-w gene u
<b>.</b> .	7770	00 1	л В 1	20	AAX25132	Human bcl-w gene.
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AAD15284 AAN81292 AAX333184		AAX3318	AAH452 AAO498		AAS0025				AAS15189		AAQ81698						AAI	AAK	AAK1	ABA32370	ABA6526	ABA4738	ABL3	ABL3	AAV5	AAV41925	
Human BC1-2 PIOCE-2 Sequence of bC1-2 Base sequence of t		Bcl-2 DNA fragment Human oncogene bcl	BCl-2. Homo sapie	3 3 3	LFn-Bcl-xL (tran	DNA encoding human	t godinate assets of the solution of the solut	Human BC1-xL nucre		x gene. H	gene. Hom	uman thymns BCL-X	MUCAIIC DCL AD COST	Rat Wild-type ber	e #5951 u	#14124 USEG	#10104	#10160 for	brain	# LOCUC FOR	#10836 for	footal Diedac	Timilarie ale	i minute	Secreta	potential potential	ν.

## ALIGNMENTS

Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer; diagnosis; degenerative disease; ss. Human bcl-w DNA. 22-APR-1998 (first entry) AAT96577; Homo sapiens. Adams JM, Cory S, Gibson LM, Holmgreen SP; WO9735971-A1. (AMRA-) AMRAD OPERATIONS PTY LTD. 27-MAR-1996; 27-MAR-1997; 02-OCT-1997. 96AU-0008965. 97WO-AU00199 Location/Qualifiers /product= bcl-w /\*tag= ದ

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Up regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis,
                                                        541
                                                                             541 9999ccct99taact9ta9999ccttttttgcta9caagtgaa 583
                                                                                                                                                                                      421 agtgggggctgggggggttcacagctctatacggggacggggccctggaggaggcgcgg
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                                                                                                                                                                                                                                                                                      Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody production or screening of potential modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW36047
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99.5%;
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AAX25134 ID AAX2

AAX25134 standard; DNA; 583 BP

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                                                                                                                                                                                                                                                                                                 Matches
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241 caggtctccgacgaactttttcaagggggccccaactggggccgccttgtagccttcttt 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 36; 52pp; English
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The present sequence is the human bcl-w gene encoding Bcl-w protein (see AAY05530), a pro-survival member of the Bcl-2 family which is contial for spermatogenesis. The clivention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility, or animals. Methods are provided for the treatment of infertility, or contains. Methods are provided for the treatment of infertility, or contains and contains a mutation is at least one allele of the human or mutation bcl-w gene or in a gene associated with bcl-w. Such animals make bcl-w gene or in a gene associated with bcl-w. Such animals infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-1999
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                                                                                                                            ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis;
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Pred. No. 3.7e-134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders
                                                                                                           421 agtgggggctgggagttcacagctctatacggggacggggccctggaggaggaggcgcg 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression in vivo. Also, antisense const where prevention of cell death is desired.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Column 15/16; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
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11-FEB-1997;
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CC specification also describes rat bel-y protein (Rbcl-y). Rbcl-y and CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y CC proteins may be used to treat conditions associated with a disruption of CC the cell death pathway. If they act as cell death inhibitors, they may be CC used in therapies to treat subjects suffering from: strokes, head trauma, CC (especially multiple sclerosis), myocardial infarction, vitally induced CC (ell death, aging, spinal cord injuries and amyotrophic lateral CC sclerosis conditions where cells under go premature cell death as a CC result of triggers which may or may not be apparent. They may also be CC used in this way to develop cell lines which remain viable in culture for CC an extended period. In contrast, if they act as cell death stimulators, CC prolonged cell life span such as cancer (especially kaposi's sarcoma and CC lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
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Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
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11-FEB-1997;
25-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW97392.
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11-FEB-1997;
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97US-0798897.
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/note= "No stop codon given"
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AAX15945

AAX15945 standard; cDNA; 579

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Column 13/14; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW61391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccagccaacgcttcacc 240
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                                                                                                                                                                                                                                                                                                     gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagccattggtggga
                                                                                                                                                                                                                                                                                                                      gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
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                                                                                                                             cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg
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Pred. No. 9.6e-122;
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20-MAY-1999 (first entry)

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                                                                                                                                                                                                                                                                                                                             The present sequence encodes rat bcl-y protein (Rbcl-y). The specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y CC proteins may be used to treat conditions associated with a disruption of CC used in therapies to treat subjects suffering from: strokes, head trauma, CC (especially multiple sclerosis), myocardial infarction, vitally induced CC ell death, aging, spinal cord injuries and amyotrophic lateral CC sclerosis- conditions where cells under go premature cell death as a CC used in this way to develop cell lines which remain viable in culture for Rhcl-v and Hhcl-v may he used to treat conditions second lines and coll death as a coll death as a coll death says to develop cell lines which remain viable in culture for Rhcl-v and Hhcl-v may he used to treat conditions as a cell death stimulators,
                                                                                                                                                                                                                                Matches 547;
                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                               Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                             Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
121 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Columns 13-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel bcl-y homologues of the rat and human bcl-2 protein for modulating programmed cell death
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                            61 aagetgaggcagaagggttatgtetgtggagetggeeeegggggagggeeeageagetgae 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COCE-) COCENSYS INC
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11-FEB-1997;
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                                                        aagctgagacagaagggttatgtctgtggagctggccctggggaaggcccagcagccgac 120
                                                                                                                                   atggcgaccccagcctcaaccccagacacacgggctctagtggctgactttgtaggctat 60
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                                                                                                                                                                                                                                          90.5%;
                                                                                                                                                                                                              Score 527.8; DB 20;
Pred. No. 9.6e-122;
""smatches 32;
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                                                                                                                                                                                                                    Indels
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The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see ANYO5531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or
                                                                                                                         Claim 3; Page 34; 52pp; English.
                                                                                                                                                           An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                         protein associated with
                                                                                                                                                                                                                WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                      16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                 16-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  animal model;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse bcl-w gene
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                                                                                                                                                                                                                                          Cory S, Gibson L,
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                                                                                                                                                         Bcl-w
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for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or model carries a mutation is at least one allele of the human or murine bcl-w gene or in a gene associated with bcl-w. Such animal have disorganised seminferous tubules and are substantially have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;
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                                                                                                                                                          AAT96578 standard; DNA; 581 BP
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                                                 Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                           541 ggggccctggtaactgtaggggccttttttgctagcaagtg
                                                                                                                                                                                                                                         541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
                                                                                                         22-APR-1998
                                       diagnosis;
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                                                                                                                                                                                                                                                                               cgtctgcgggagggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg
                                                                                                                                                                                                                                                                                              cgtctgcgggagggaactgggcatcagtgaggacagtgctgacgggggccgtggcactg 540
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                                        degenerative disease; ss.
                                                                                                          (first entry)
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94.1%;
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Pred. No. 1.9e-121;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family. This gene promotes cell survival, so its modulation is useful in family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, bypoxia, ischaemia, human immunodeficiency virus infection or in cell hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell transplants. Up-regulation of develop new lines, to facilitate lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w during genetic modification. It can be used to produce recombinant Bcl-w during denetic modification. It can be used to produce recombinant Bcl-w during denetic modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams JM, Cory S, Gibson LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 50-51; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                degenerative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modulators
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                                                                                                                                                                                                                                                                                                                                   61 aagetgaggeagaagggttatgtetgtggagetggeeegggggagggeeeageagetgae 120
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                                                                                                                                                                                                                                                      ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                            caggtotocgacgaactttttcaagggggcoccaactggggcocccttgtagccttottt 300
                                                                                caggittccgacgaacttttccaagggggccctaactggggccgtcttgtggcattctt 300
                                                                                                                                                                                        ttototgacotggcogotcagotacacgtgacoccaggctcagoccagcaacgcttcacc 240
                                                               gtotttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga
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/note= "q"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.8%;
91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 505.8; DB 18
Pred. No. 2.8e-116;
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                                                     fertility, by modulating spermatogenesis. An animal specific spene associated with bcl-w. Such animals have disorganised other major abnormalities as determined by infertile, but possess no They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise that the sequences of the sequen
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                                                                                                                                                                                                             The present sequence is described as a derivative of the mouse bcl-w gene (see AAX25133) and encodes Bcl-w protein (see AAY05533), and which is essential for spermatogenesis. The invention relates identification of molecules and general to an animal model for the inducing or reducing fertility of male animals. Methods are fertility, by modulating spermatogenesis. An animal model carries a mutation of the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries
                                             facilitating spermatogenesis in animals, or which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 38; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams J, Cory S, Gibson L,
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Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

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  21-JAN-1997;
                           21-JAN-1998;
                                                    23-JUL-1998.
                                                                             W09831800-A2.
                                                                                                                                                                         Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent; s
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                 Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                  20-NOV-1998 (first entry)
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                                                                                                                                                                                                                                                                                   AAV41925;
                                                                                                                                                                                                                                                                                                AAV41925 standard; cDNA; 1098 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                        541 ggggccctggtaactgtaggggccttttttgctagcaagtg 581
                                                                                                                                                                                                                                                                                                                                                                       541 9999ccctggtaactgtaggggccttttttgctagcaagtg 581
                                                                                                                                                                                                                                                                                                                                                                                                                 481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
                                                                                                                                                                                                                                                                                                                                                                                                   481 cgtctgcgggagggcaactgggcatgagtgagcacagtggtgacggggggccgtggcactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 agtggcggctgggcggacttcacagctctatacggggacggggccctggaggacgcacgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atgeogaceeeageeteaaeeeeagaeaeaegegetetagtggetgaetttgtaggetat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534;
97US-0034205
                       98WO-US00960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                        /product= "Bcl-like (HAICH29) protein"
                                                                                                                                      Location/Qualifiers
                                                                                                                            .1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 505.8; DB 20; Length 581; Pred, No. 2.8e-116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
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Best Local S
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                                                      AAV59630
                                                               RESULT
DX AX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AUCK-) AUCKLAND UNISERVICES LTD. (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used in the method of the invention. The products of the cione can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                           121 ccgctgcaccaagccatgcgggcagctggagatgagttcgaggacccgcttccggcgcacc 180
                                                                                                                                                                                                                                                                                 AAV59630 standard; DNA; 1864 BP
                                                                                                                                                                                                                                                                                                                  121
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                       AAV59630;
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                                                                                                          421 agtgggggctgg 432
                                                                                                                                        361
                                                                                               421 agtgggggctgg 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is the nucleotide sequence of the cDNA clone Bcl-like (HAICH29), in the method of the invention. The products of the clone can be
                                                                                                                                                                                                                                                                                                                                                                     aagctgaggcagaagggttatgtctgtggagctggcccgggggagggcccagcagctgac 120
                                                                                                                                                                                                                                                                                                                                                                                                    atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                                                                                                                                                                 ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                                                                                                                                      ttetetgatetggeggeteagetgcatgtgaceceaggeteageceaacaacgetteace
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                                                                                                                                                   gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 428.8; DB 19; Length 1098; Pred. No. 4.2e-97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                  07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
                                                                                                                11 APR-1997
23 -MAY-1997
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11-APR-1997;
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                                        23-MAY-1997;
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97US-0043313
97US-0043314
97US-0043568
97US-0043576
97US-0043576
97US-0043578
97US-0043578
97US-004369
97US-004367
97US-004367
97US-0043671
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97US-0047501.
97US-0047502.
97US-0047503.
97US-0047581.
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97US-0047584.
97US-0047585.
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97US-0047587.
97US-0047588.
97US-0047589.
97US-0047590.
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97US-0047492.
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9705-0047593.

9705-0047594.

9705-0047595.

9705-0047596.

9705-0047597.

9705-0047599.

9705-0047600.
                      97US-0047613.
97US-0047614.
97US-0047615.
97US-0047617.
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S-0047587.
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Human secreted protein gene 120 clone HGBGZ64.

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymos; osteoporosis; arthritis; testis; lung; thyroid;tis; thyroid; digestion; osteoporosis; arthritis; testis; lung; thyroid; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

19-JAN-1999 (first entry)

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from the human cDNA clone HGBGZ64 (deposited as clone ATCC 97902 and ATCC 209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human the fusion proteins by linking to the gene to a human the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic which are useful for preventing, treating or ameliorating medical medical manufactures and their fragments (nucleic which are useful for preventing, treating or ameliorating medical
conditions e.g. by protein or gene therapy. Also, pathological
                                                                                                                                                                                                                      New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological
                                                                                                                                                                               Claim 1; Page 353-354; 721pp; English.
                                                                                                                                                                                                            disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                     Feng P,
Kyaw H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-1997
22-AUG-1997
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                                                                                                                                                                                                                                                                                          P-PSDB; AAW74848
                                                                                                                                                                                                                                                                                                                                                                                    Bednarik DP,
                                                                                                                                                                                                                                                                                                                                         Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUN-1997;
                                                                                                                                         sequence represents a nucleic acid molecule designated Gene 120
                                                                                                                                                                                                                                                                                                                               Lafleur DW, Li Y, N
                                                                                                                                                                                                                                                                                                                                                                   Ferrie AM,
                                                                                                                                                                                                                                                                                                                                                                               Brewer LA,
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97US-0057669.
97US-0057761.
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97US-0056878.
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97US-0056876.
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97US-0047632.
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97US-0048974
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Fischer CL, Florence KA, Greene JM,
, Li Y, Moore PA, Ni J, Olsen HS,
Soppet DR, Young PE, Yu GL, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                    Greene JM,
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RESULT 13
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02-JUL-2001; 2001WO-EP07537
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                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local !
                                                                  WO200200928-A2
                                                                                                                             neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                HOMO sapiens
                                                                                                                                                                                                                       Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO: 201.
                                                                                                                                                                                                                                                                                                                                                          ABL32228 standard; DNA; 6049 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                       431 agtgggggctgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV59511 for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 ccgctgcaccaagccatgcgggcagckggagatgagttcgagacccgcttccggcgcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1864 BP; 494 A; 403 C; 506 G; 455 T; 6 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agtgggggctgg 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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99.3%;

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _DB 19; Length 1864;
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RESULT 14
ABL3229/c
ID ABL322
XX
AC ABL322
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AC ABL322
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DE Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6049 BP; 1480 A; 109 C; 1549 G; 2911 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 201; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytosine methylation
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                              26-MAR-2002
                                                           ABL32229
                                                                                       ABL32229 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  tcgttgtattaagttatgcgggtagttggagatgagttcgagattcgttttcggcgtatt 5180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aagttgaggtagaagggttatgtttgtggagttggtttcgggggagggtttagtagttgat 5120
                                                                                                                                                                                                                   caggtctccgacgaactttttcaagggggccccaactggggccgccttgtagccttcttt
                                                                                                                                                                                                                                                                                                                                                                                           ttttttgatttggcggtttagttgtatgtgattttaggtttagtttaataacgttttatt 5240
                                                                                                                                                                                                                                                                                                                                                                                                          ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                                                                                                  gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
                                                                                                                                                                                                                                                                                                                                    agtgggggctggg 433
                                                                                                                                                                                                                                                                           323;
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Similarity 74.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000DE-1032529.
2000DE-1043826.
                              (first entry)
   system
                                                                                        DNA; 6049
    associated gene SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 257; DB 24;
Pred. No. 2.8e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
       ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute_myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 202; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6049 BP; 1591 A; 109 C; 1429 G; 2920 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1049 ATAACGACCCCAACCTCGACCCCAAACACACGAACTCTAATAACAAACTTTATAAATTAT 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases.
     749
                                                                                                                                                                                                              698
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                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                     989 AAACTAAAACAAAAAATTATATCTATAAAACTAACCCCGAAAAAAACCCAACAACTAAC
                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 aagetgaggeagaagggttatgtetgtggagettggeceeggggagggeceageagetgae 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                                                                                                                                                                                                ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
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gtctttggggctgcactgtgtgctgagagtgtcaaccaaggagatggaacccactggtggga
                                                                                                                                    caggtotocgacgaactttttcaaggggggccccaactggggccgccttgtagccttcttt 300
                                                                                                                                                                                                            TTCTCTAATCTAACGACTCAACTACATATAACCCCAAACTCAACCCCAACAACGCTTCACC
                                                                                                                                                                                                                                             ttototgatotggoggotoagotgcatgtgacocoaggotoagocoagoaacgottoaco
                                                                                                                                                                                                                                                                                                                    CCGCTACACCAAACCATACGAACAACTAAAAATAAATTCGAAACCCGCTTCCGACGCACC
                                                                                                        CAAATCTCCGATAAACTTTTTCAAAAAACCCCCAACTAAAACCGCCTTATAACCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 223; DB 24; Pred. No. 7.8e-46;
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abnormal
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RESULT 1

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KW Huma

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PN WO2(

PN 00-4

YX 30-6

PR 20-6

PR 20-6

PR 20-6

PR 20-6

PR 20-6

PR 04-6

PR 20-7

PR 2
                                 CC nucleic acid probes for measuring gene expression in a sample derived CC from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids CC derived from mRNA of human breast, and then measuring the label CC bound to each probe of the microarray. The probes are useful for CC verifying the expression of regions of genomic DNA predicted to CC encode proteins. They are useful for gene discovery, and for CC expression analysis is useful for assessing the toxicity of chemical CC expression analysis is useful for assessing the toxicity of chemical CC diversity of probes for measuring gene expression, with far less bias CC rapid production of functional information from genomic sequence. The CC resent sequence is a single exon nucleic acid probe of the invention. CC Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly considered to the patent of the method at the patent of the consideration from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000CB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; SEQ ID NO 6077; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-496933/54.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human breast cell single exon nucleic acid probe #6077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 629 AAT 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank DR;
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Query Match

25.7%;

Score

150;

DB 22;

Length 150;

Sequence 150 BP; 25 A; 33 C;

65 G;

27 T; 0 other;

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Ωy
                                                              В
                                                                                       Qy
                                                                                                                      DЬ
                                                                                                                                                Ωy
                                                                                                                                                                               Matches
                                                                                                                                                                                           Best Local Similarity
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             553 actgtaggggccttttttgctagcaagtga 582
                                                                                                                          433 gcggagttcacagctctatacggggacggggcctggaggaggcgcgcggcgtctgcggggag
                                                                                          493
                                                              61
                                                                                                            1 gcggagttcacagctctatacggggacggggccctggaggaggcgcggcgtctgcgggag
actgtagggccttttttgctagcaagtga 150
                                                    gggaactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggta 120
                                                                    gggaactgggcatcagtgaggacagtgctgacgggggccgtggcactgggggccctggta 552
                                                                                                                                                                          Conservative 0;
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); Mismatches 0;
                                                                                                                                                                          Indels
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Search completed: June Job time: 4702 sec 6 2002, 12:02:24

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Listing first 45 summaries
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1: /SIDS1/gcgdata/g
2: /SIDS1/gcgdata/g
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582
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Gapop 10.0 , Gapext 1.0
SIDSI/gcgdata/geneseq/geneseqn-embl/NA199 DAT: *
SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001 DAT: *
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	н	ength		ID	Description
1	577.8		581	20	AAX25133	Mouse bcl-w gene.
N	563.4	96.8	581	18	AAT96578	Mouse bcl-w DNA.
ω	563.4	96.8	581	20	AAX25135	Mouse bcl-w gene d
4	558.2	95.9	579	19	AAV28333	Rat bcl-y gene. R
տ	558.2	95.9	579	20	AAX15945	cDNA encoding the
σı	520.2	89.4	581	20	AAX25132	Human bcl-w gene.
7	519.6	89.3	583	18	AAT96577	Human bcl-w DNA.
8	519.6	89.3	583	20	AAX25134	Human bcl-w gene d
9	515	88.5	579	19	AAV28334	Human bcl-y gene.

45 125.8 21.6 555 22 AAI53868	44 125.8 21.6 555 22 AAK48039	43 125.8 21.6 555 22 AAK21876	125.8 21.6 555 22 ABA38761	41 125.8 21.6 555 22 ABA73433	126.6 21.8 720 22 AAH45295	39 126.8 21.8 600 22 AAI40812	126.8 21.8 600 22 AAK35096	37 126.8 21.8 600 22 AAK09207	36 126.8 21.8 600 22 ABA28894	35 126.8 21.8 600 22 ABA60917	.6 22.3 747 22 AAF30926	131.2 22.5 1455 22 AAS00250	134.6 23.1 7372 20 AAX33182	134.6 23.1 1236 22 AASO0247	134.6 23.1 926 22 AAC90810	134.6 23.1 926 22 AAS15189	134.6 23.1 926 21 AAZ93614	134.6 23.1 926 17 AAT40079	134.6 23.1 926 16 AAQ81698	134.6 23.1 702 22 AAH43464	134.6 23.1 636 22 AAH48169	135 23.2 1742 22 AAF75960	148.4 25.5 150 22 AAI05940	148.4 25.5 150 22 AAI45438	148.4 25.5 150 22 AAI20236	148.4 25.5 150 22 AAK39424	148.4 25.5 150 22 AAK13683	48.4 25.5 150 22 ABA32370	148.4 25.5 150 22 ABA65269	15 148.4 25.5 150 22 ABA47382	192.6 33.1 6049 24 ABL32229	218.6 37.6 6049 24 ABL32228	372.4 64.0 1864 19 AAV59630	2.8 64.1 1098 19 AAV41925	
Probe #22554 used	Human bone marrow	Human brain expres	101 /77/T#	TETACI	ncoaing		bone			roetal		LFn-Bcl-X1 apoptos	Base sequence of t		Human Bc1-xL nucle	Human bcl-x cDNA.		·	n thymus B	20356	Mutant bc1-XL cod1	_	Probe #5931 used t	Probe #14124 used		bone ma	Human brain expres	for				Human immune syste	Human secreted pro	Nucleofide sequenc	

## ALIGNMENTS

XX TT	DR X	P1 XX	PA	PR	X P X	PD	X PX	X	SO	XX	ΚW	ΚW	XX	DE ?	¥ F	X	AC	XX	Ħ	AAX25133	RESULT
An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w	WPI; 1999-243890/20.	Adams J, Cory S, Gibson L, Koentgen F, Print C;	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.	16-SEP-1997; 97AU-0009228.	16-SEP-1998; 98WO-AU00764.	25-MAR-1999.	WO9913710-A1.		Mus sp.		animal model; ss.	Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;		Mouse bcl-w gene.	02-70F-1333 (IIISt ently)		AAX25133;		AAX25133 standard; DNA; 581 BP.	33	

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RESULT
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 AAT96578
                                AAT96578 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the mouse bcl-w gene encoding Bcl-w protein (see AAY05531), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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99.7%;
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Best Local S
Matches 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl-w; apop
diagnosis;
                                                                                                                                                                                                                                                                                                                        Sequence 581
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                                         ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc
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570; Conser
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sis; degenerative disease; ss.
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98.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis related gene bcl-w - used to induce val, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                        164 C;
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Pred. No. 2.
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                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse bc1-w gene derivative
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The present sequence is described as a derivative of the mouse bcl-w gene (see AAX25133) and encodes Bcl-w protein (see AAX95533), pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries fertility, is at least one allele of the human or murine bcl-w gene
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                                                                                                                                                                              An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                      P-PSDB; AAY05533
                                                                                                                                                                                                                                    WPI; 1999-243890/20.
                                                                                                                                                    Disclosure; Page 38; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no seminferous tubules and are substantially infertile, but possess no
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                                                                                   bc1-2; cell death pathway; apoptotic; apoptosis;
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                             Location/Qualifiers
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Pred. No. 2.5e-141;
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                                                                          361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression in vivo. Also, antisense const where prevention of cell death is desired.
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97US-0798897.
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97.8%;
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Pred. No. 6.1
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Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;

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CC The present sequence encodes rat bcl-y protein (Rbcl-y). The Specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y CC proteins may be used to treat conditions associated with a disruption of CC used in therapies to treat subjects suffering from: strokes, head trauma, CC (especially multiple sclerosis), myocardial infarction, vitally induced CC (especially multiple sclerosis), myocardial infarction, vitally induced CC cell death, aging, spinal cord injuries and amyotrophic lateral CC cresult of triggers which may or may not be apparent. They may also be CC used in this way to develop cell lines which remain viable in culture for CC an extended period. In contrast, if they act as cell death stimulators, CC Rbcl-y and Hbcl-y may be used to treat conditions associated with CC prolonged cell life span such as cancer (especially kaposi's sarcoma and CC lung cancer) and auto/hyperimmune diseases. They may also be used to
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11-FEB-1997;
25-NOV-1997;
                          cause cell death in, and hence control, parasites.
                                        lung cancer) and auto/hyperimmune diseases. They may also be used to
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Columns 13-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel bcl-y homologues of the rat and human bcl-2 protein for modulating programmed cell death
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COCE-) COCENSYS INC.
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             Adams J, Cory S,
                                   (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
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Pred. No. 6.1e-140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the human bcl-w gene encoding Bcl-w protein (see AAY05530), a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 32; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in
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93.5%;
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Pred. No. 9.2e-130;
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AAT96577
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                                                                                                                                                                                                                                                                                                                 auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
                                                                                                                                                                                                                                                                                           Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc
                                              121 ccgctgcaccaagccatgcggggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene family, extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              degenerative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
diagnosis; degenerative disease; ss.
                                                                                                          61 aggetgaggeaggaggttatgtetgtggagetggeeetgggggaaggeeeageegee 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human bcl-w DNA
                                                                                                                                                    1 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 60
                                                                                                                                                                     1 atggcgaccccagcctcaaccccagacaccacgggctctagtggctgactttgtaggctat 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT96577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT96577 standard; DNA;
                                                                                                                                                                                                                                           Local Similarity
                                ccgctgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997-489635/45.
                                                                                                                                                                                                                         543; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96AU-0008965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-AU00199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= bcl-w
                                                                                                                                                                                                                                    93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gibson LM, Holmgreen SP;
                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                               Score 519.6; DB 18
Pred. No. 1.3e-129;
                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                              DB_18; Length 583;
                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                    Indels
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           The present sequence is described as a derivative of the human bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the inducing or reducing fertility of male animals. Wethods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries
    fertility, by modulating spermatogenesis. a mutation is at least one allele of the
                                                                                                                                                                                                  An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                        Disclosure; Page 36; 52pp; English.
                                                                                                                                                                                                                                                     P-PSDB; AAY05532
                                                                                                                                                                                                                                                                  WPI; 1999-243890/20.
                                                                                                                                                                                                                                                                                               Adams J, Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09913710-A1.
                                                                                                                                                                                                                                                                                                                         (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                             16-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                animal model;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human bcl-w gene derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX25134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 9999ccctggtaactgtagggggctttttttgctagcaagtga 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 cgtctgcgggagggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                       98WO-AU00764
                                                                                                                                                                                                                                                                                              Gibson L,
                                                                                                                                                                                                                                                                                            Koentgen F, Print C;
the human or murine bcl-w gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540
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FT SXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 aagetgaggcagaagggttatgtetgtggagetggeeegggggagggeeeageagetgae 120
                                                                                                                                                 02-OCT-1998 (first entry)
                                                                                                                                                                                AAV28334;
                                                                                                                                                                                                          AAV28334 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                           421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ctctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
                                                                                      ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human
                                                                                                                     Human bcl-y gene
                                                                                                                                                                                                                                                                                                   1 atggcgaccccagcctcggccccagacacacgggctctggtggcágactttgtaggttat 60
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                                                                                                                                                                                                                                                                                  541 ggggccctggtaactgtaggggccttttttgctagcaagtga 582
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                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttctctgacctggccgctcagctacacgtgaccccaggctcagcccaggcaacgcttcacc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    543;
                                                                                                                                                                                                                                                                                                                                                                                                                        agtggcggctgggcggagttcacagctctatacggggacgggggccctggaggaggaggcacgg 480
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                                                                                                                                                                                                                                                                                                                                               cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
                                                                                                                                                                                                                                                                                                                                                              cgtctgcgggaggggaactgggcatcagtgaggacagtgctgacggggggccgtggcactg
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                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 519.6; DB 20
pred. No. 1.3e-129;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The mammalian bcl-y genes encode a protein that is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct be used to prevent uncontrolled cell growth, either by its direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Column 15/16; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth e.g. cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in diwhere prevention of cell death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;
                                                                                                                                                                                                                                                                                         121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                              241 caggittccgacgaactittccaagggggccctaactggggccgtcttgtgggcattcttt 300
                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                121
             421 agtggcggctgggcggagttcacagctctatacggggacggggccctggaggaggacgg 480
                                                                  361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
                                                                                                          301 gtctttggggctgcactgtgtgctgagagtgtcaacaaggagatggaaccactggtggga
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                                                                                                                                                                                                                                                                                                                                  61 aagctgaggcagaagggttatgtctgtggagctggccccgggggagggcccagcagctgac 120
                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
   421
                                                    1 atggcgaccccagcctcaaccccagacacacgggctctagtggctgtattgtaggctat 60
                                                                                                                                                                                                                                                                                                                                                                                        1 atggcgaccccagcctcggccccagacacacgggctctggtggaagactttgtaggttat 60
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                                                                                                                                                                                                                                                                             ccactgcaccaagccatgcgggcagctggagatgagttcgagacccgcttccggcgcacc
                                                                                                                                                                 caggtctccgatgaactttttcaagggggccccaactgggggccgccttgtagccttcttt
agtgggggctgggcggagttcacagctctatacggggacggggccctggaggaggcgcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0798897
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/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.5%;
93.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 515; DB 19;
Pred. No. 2.3e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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     Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced sclerosis conditions where cells under go premature cell death as a used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they act as cell death stimulators, prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                               The present sequence encodes human bcl-y protein (Hbcl-y). The specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: Strokes, head trauma, and the conditions associated with a disruption of used in therapies to treat subjects suffering from: Strokes, head trauma,
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11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Columns 15-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               Novel bcl-y homologues of the rat and human bcl-2 protein for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW97392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding the human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX15946 standard; cDNA; 579 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX15946;
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97US-0798897.
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Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

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AAV41925
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                            21-JAN-1998;
                                                                                        W09831800-A2.
                                                                                                                                                                                                                            Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                            Nucleotide sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                             immunological disorder; autoimmune disease; anti-infectious agent; ss
                                                                                                                                                                                                                                                                                                                                                         AAV41925 standard; cDNA; 1098 BP
                                                                                                                                                                                                                                                                                                 20-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             541 ggggccctggtaactgtaggggccttttttgctagcaag 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ccgctgcaccaagccatgcgggctgctgqgagacgagtttgagacccgtttccgccgcacc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 aagctgaggcagaagggttatgtctgtggagctggccccggggagggcccagcagctgac 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                         98WO-US00960
                                                                                                           /product= "Bcl-like (HAICH29) protein"
                                                                                                                               /*tag=
                                                                                                                                                               Location/Qualifiers
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93.1%;
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Pred. No. 2.3e-128;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1098 BP; 264 A; 279 C; 325 G; 230 T; 0 other;
                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                        121
                                        AAV59630 standard; DNA; 1864 BP.
 19-JAN-1999
                      AAV59630;
                                                                                                                                      361
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                                                                                                                                                                                       301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krissansen GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                             64.1%;
91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 372.8; DB 19; Pred. No. 3.4e-90; Pred. No. 3.4e-90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1098;
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cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein gene 120 clone HGBGZ64.
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07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
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23-MAY-1997;
23-MA
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07-MAR-1997;
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11-APR-1997;
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97US-0047501.
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97US-0047503.
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97US-0047582.
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97US-0047584

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97US-0047589

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97US-0047592

97US-0047593

97US-0047595

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      97US-0047614.
97US-0047615.
97US-0047617.
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97US-0047492.
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97US-0047613
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S-0043311.
S-0043312.
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ATCC 209048) which encodes a secreted human protein. The gene can be used to generate fusion proteins by linking to the gene to a human finmunoglobulin Fc portion (e.g. AAV59502) for increasing the stability the fused protein as compared to the human protein only. The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological
                                                                                                                                                                   New isolated human genes and the secreted polypeptide(s) they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1997
                                                                                                                                               Claim 1; Page 353-354; 721pp; English.
                                                                                                                                                                                                                                                                               Feng P,
Kyaw H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1997
22-AUG-1997
                                                                                                                                                                                                                                                                                                        Bednarik DP,
                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-1997;
23-MAY-1997;
                                                                                         sequence represents a nucleic acid molecule designated Gene 120 the human cDNA clone HGBGZ64 (deposited as clone ATCC 97902 and 209048) which encodes a secreted human protein. The gene can be
                                                                                                                                                                                                                                        1998-506364/43.
                                                                                                                                                                                                                               AAW74848
                                                                                                                                                                                                                                                                Lafleur DW,
f, Shi Y, Sc
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97US-0056910.
97US-0056911.
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97US-0056862
97US-0056862
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97US-0056872
97US-0056872
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97US-0057669.
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97US-0056637.
97US-0056662.
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97US-0056884.
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970S-0056880
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                                                                                                                                                                                                                                                                        Fischer CL, Flor
, Li Y, Moore PA,
                                                                                                                                                                                                                                                          Carter KC, Duan R, Ebner R, Enher CL, Florence KA, Greene JM, Y, Moore PA, Ni J, Olsen HS, IDR, Young PE, Yu GL, Zeng Z;
                                                                                                                                                                                                                                                                                              Endress GA;
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ABL32228
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                                                                                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemacute myeloid leukaemia; Alzheimer's disease; ALDS; epilepsy;
        02-JUL-2001; 2001WO-EP07537.
                                          03-JAN-2002.
                                                                                                                                      neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                    WO200200928-A2
                                                                                                    Homo sapiens.
                                                                                                                                                                                                                              Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                     ABL32228;
                                                                                                                                                                                                                                                                                                                                                            ABL32228 standard; DNA; 6049 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                      431 agtgggggctgg 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 agtggcggctgg 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 caggtctccgatgaactttttcaagggggccccaactggggccgccttgtagccttcttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (see AAV59511 for described uses).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ccgctgcaccaagccatgcgggctgctggagacgagtttgagacccgtttccgccgcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 aagctgaggcagaagggttatgtctgtggagctggccccgggggagggcccagcagctgac 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 atggcgaccccagcctcggccccagacacacgggctctggtggcagactttgtaggttat 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc
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                                                                                                                                                                                                                                                               immune system associated gene SEQ ID NO: 201.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggotgaggcagaagggttatgtotgtggagotggcotggggaaggcocagcogocgac 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttctctgatctggcggctcagctgcatgtgaccccaggctcagcccaacaacgcttcacc
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91.2%;
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Pred. No. 5.1
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                                                                                                                                                                     anaemia;
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ABL32229/c
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Best Local
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01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 201; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5121
                                                                                                                                                                                                  5421 agtgggggttggg 5433
                                                                                                                                                                                                                                                                                                                               241 caggtttccgacgaccttttccaagggggccctaactggggccgtcttgtgggcattcttt 300
Human immune system associated gene SEQ ID NO:
                                                                              ABL32229 standard; DNA; 6049
                                                       ABL32229;
                           26-MAR-2002 (first entry)
                                                                                                                                                                                                                  361 caagtgcaggattggatggtggcctacctggagacacgtctggctgactggatccacagc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 agtggcggctggg 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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2000DE-1043826.
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69.1%;
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                                                                                      BP
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Matches 279;
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acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acure myerora reukaemna; Alzhelmer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 202; 32pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6049 BP; 1591 A; 109 C; 1429 G; 2920 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                         686
                                                                                                                                                                                                                                                                                                                                                      121
809 CAAATCTCCGATAAACTTTTTCAAAAAAACCCCAACTAAAACCGCCTTATAACCTTCTTT 750
                                                                                                                                         241 caggittccgacgaacttttccaagggggccctaactgggggccgtcttgtgggcattcttt 300
                                                                                                                                                                                                                               181 ttctctgacctggccgctcagctacacgtgaccccaggctcagcccagcaacgcttcacc 240
                        301 gtctttggggctgccctgtgtgctgagagtgtcaacaaagaaatggagcctttggtggga 360
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                                                                                                                                                                                                                                                                                                   CCGCTACACCAAACCATACGAACAACTAAAAATAAATTCGAAACCCGCTTCCGACGCACC
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2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.1%;
66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 192.6; DB pred. No. 1e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24; Length 6049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144; Indels
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The invention relates to a spatially-addressable set of single exon convolete acid probes for measuring gene expression in a sample derived from human breast and Br 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids convolved from mRNA of human breast, and then measuring the label convolved from the expression of regions of genomic DNA predicted to convolving the expression of regions of genomic DNA predicted to convolving the expression of regions of genomic DNA predicted to convolving the expression and/or prognosing breast disease. Gene capter of the expression and/or prognosing breast disease. Gene convolving the probes of the microarray of this invention presents a far greater convolving to probes for measuring gene expression, with far less bias convolving production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Convolving the production, but was obtained in electronic format directly convolving the production of the property of the sequence data for this patent did not form part of the convolving production of the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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ABA47382
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SSP-2000; 2000US-0234687

27-SEP-2000; 2000US-023559.

04-OCT-2000; 2000GB-0024263.
                       from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; SEQ ID NO 6077; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human breast cell single exon nucleic acid probe #6077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA47382 standard; DNA; 150 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
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Query Match

25.5%; Score 148.4; DB 22; Length 150;

Sequence 150 BP; 25 A; 33 C; 65 G; 27 T; 0 other;

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                                  QΥ
                                                                Вb
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Matches 149; Conserv
121 actgtaggggccttttttgctagcaagtga 150
               553 actgtaggggccttttttgctagcaagtga 582
                                                                493 999aactgggcatcagtgaggacagtgctgacggggggccgtggcactggggggccctggta 552
                                                                                                                        433 goggagttcacagctctatacggggacggggccctggaggaggaggcacggcgtctgcgggag 492
                                                 61 gggaactgggcatcagtgaggacagtgctgacgggggccgtggcactggggccctggta 120
                                                                                                       Conservative
                                                                                                                                                                                     99.38;
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                                                                                                                                                                     Pred. No. 2.4e-30; 0; Mismatches 1;
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                                                                                                                                                                Gaps
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Search completed: June Job time: 4709 sec 6, 2002, 12:02:31

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